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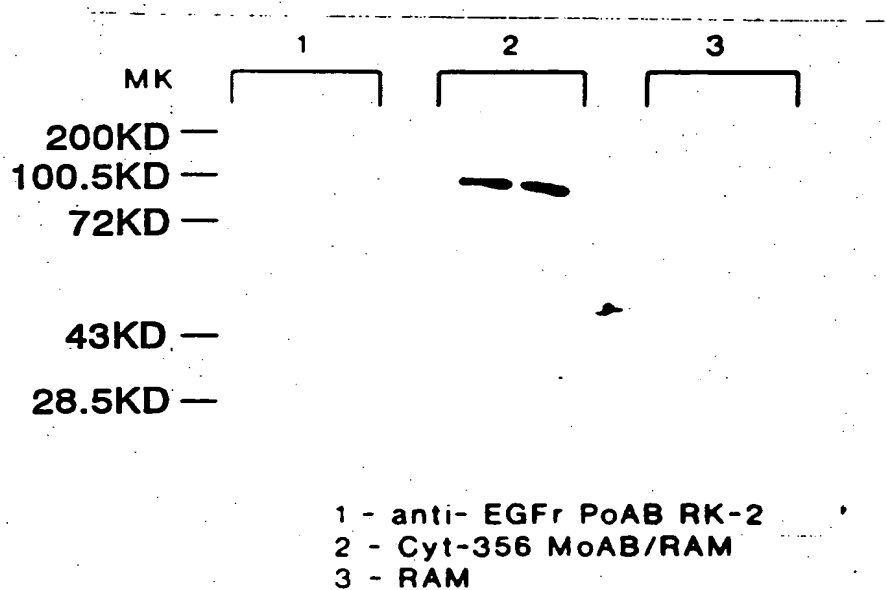
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1/130

FIGURE 1



2/130

FIGURE 2B

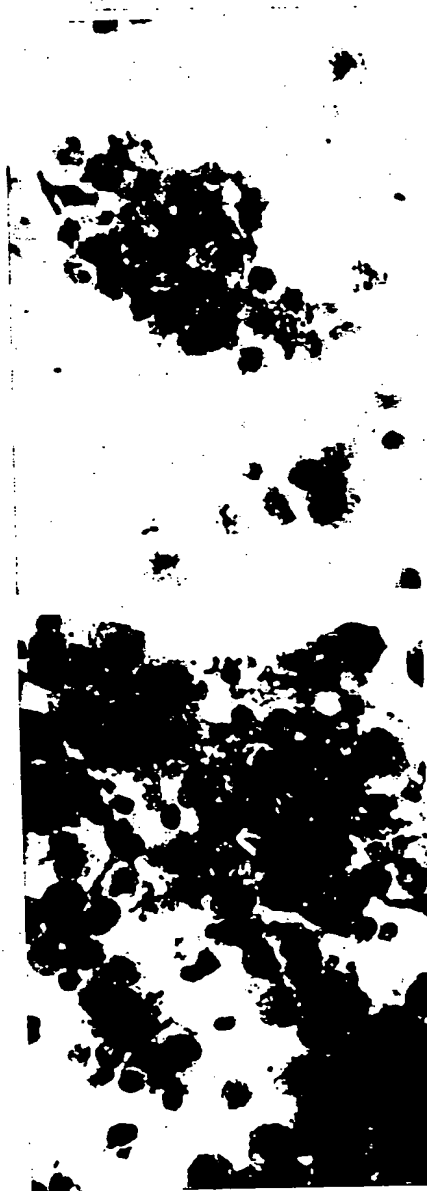


FIGURE 2A

FIGURE 2D



FIGURE 2C

3/130

FIGURE 3B



FIGURE 3A



FIGURE 3D

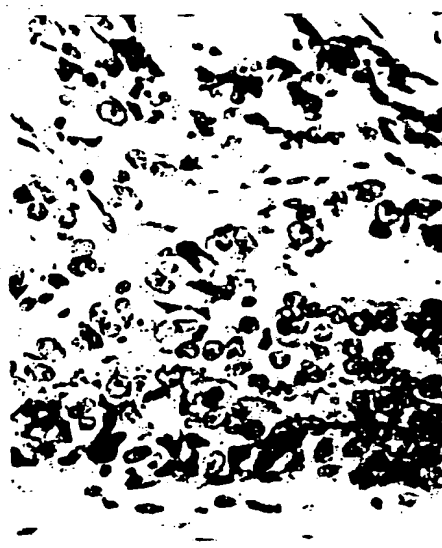
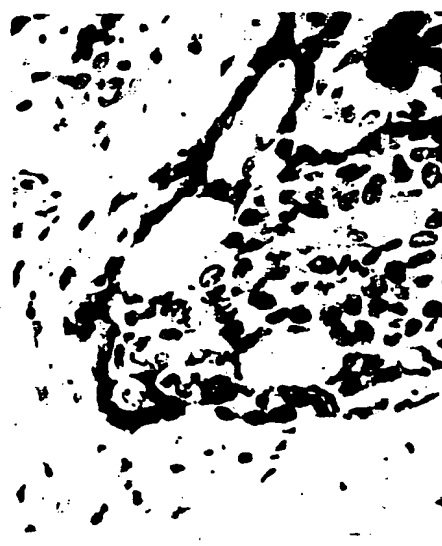


FIGURE 3C



4/130

FIGURE 4

100.5 ——— [REDACTED]

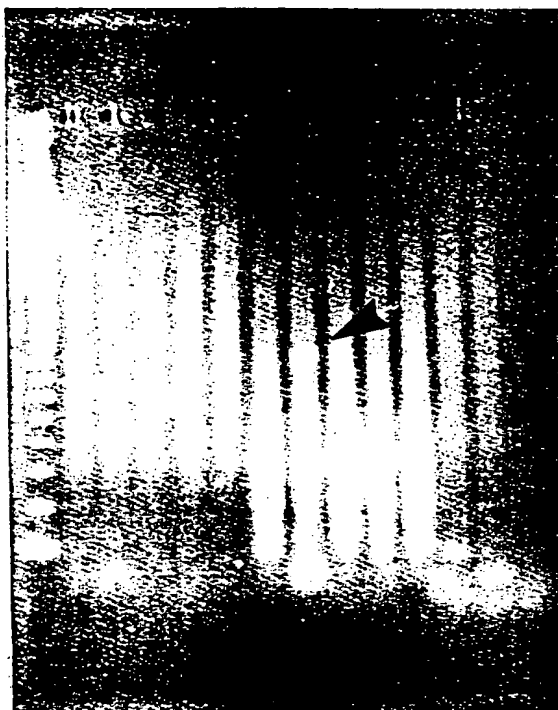
72.0 ———

43.0 ———

28.5 ———

5/130

FIGURE 5



6/130

FIGURE 6A

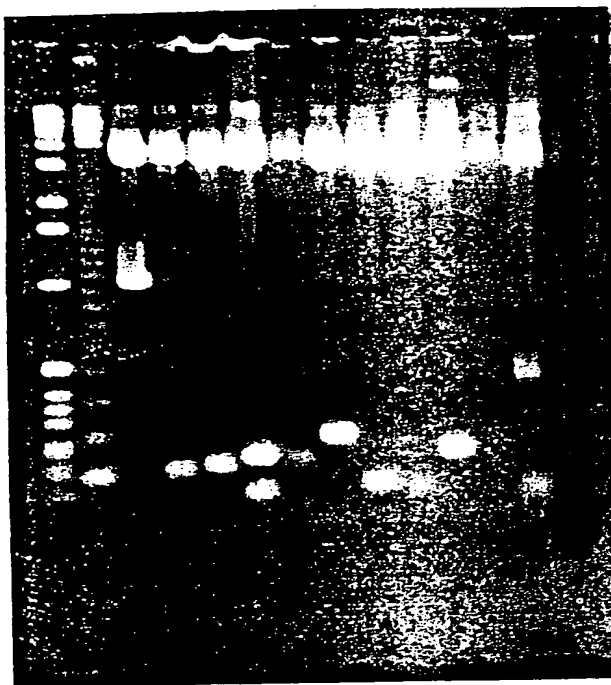
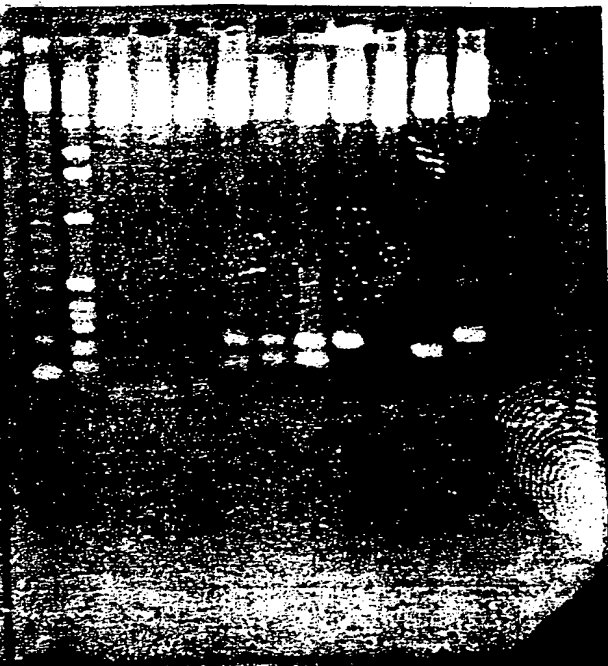
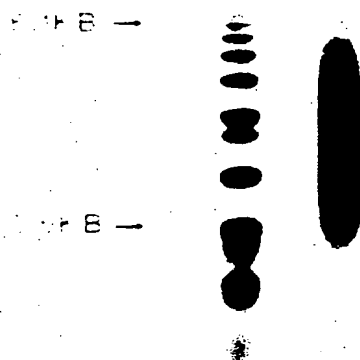


FIGURE 6B



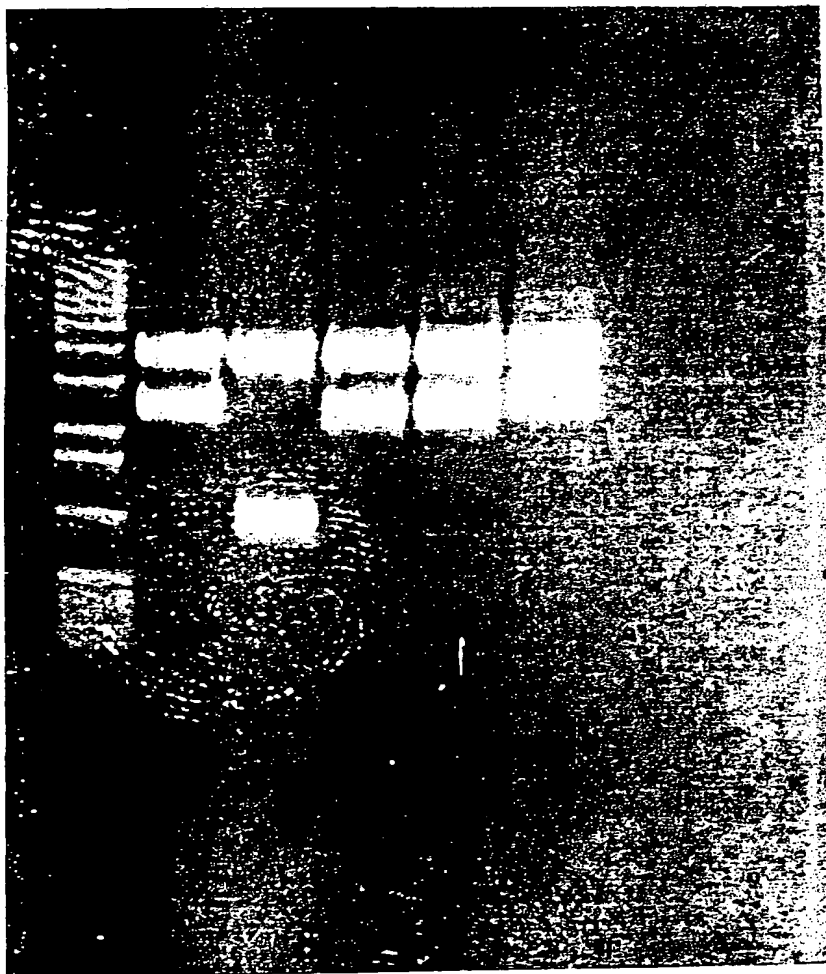
7/130

FIGURE 7



8/130

FIGURE 8



9/130

FIGURE 9

4 —
3 —
2 —
1.6 —

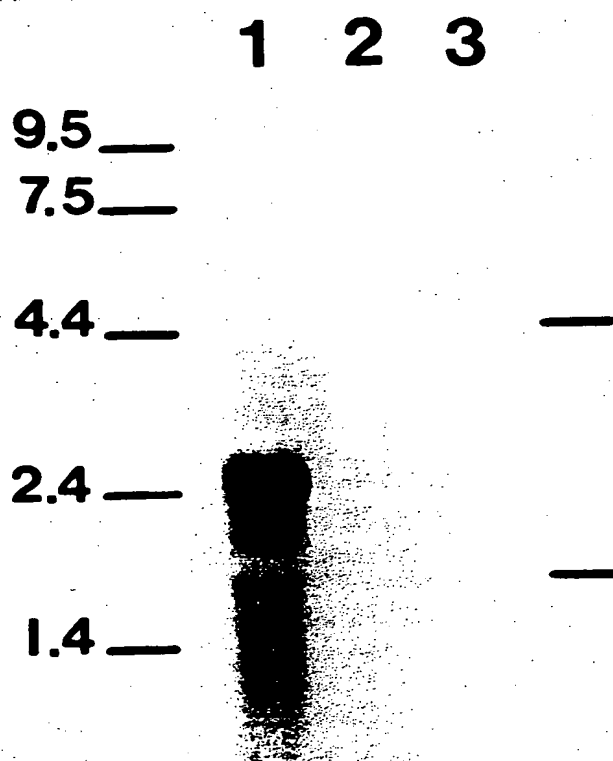
10/130

FIGURE 10



11/130

FIGURE 11



12/130

FIGURE 12A

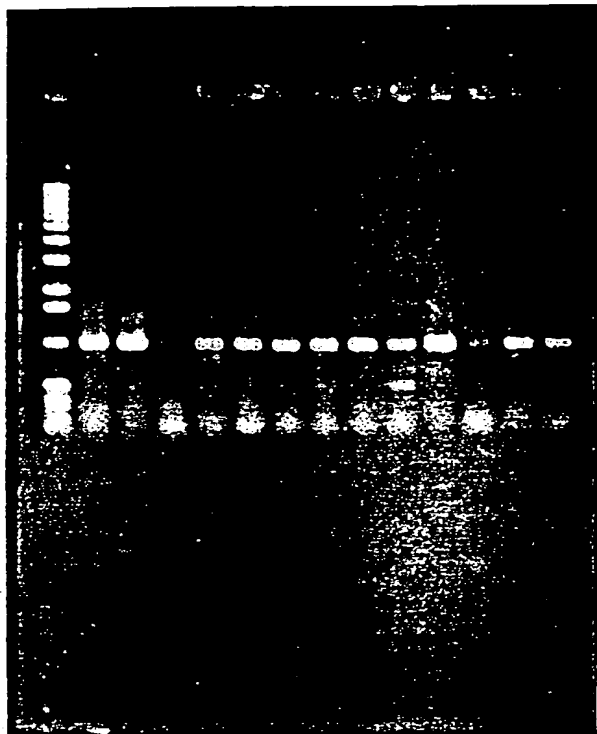
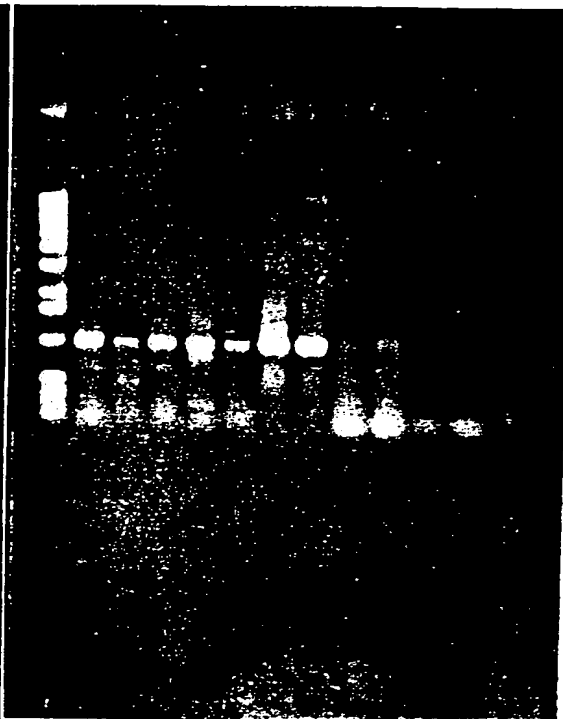
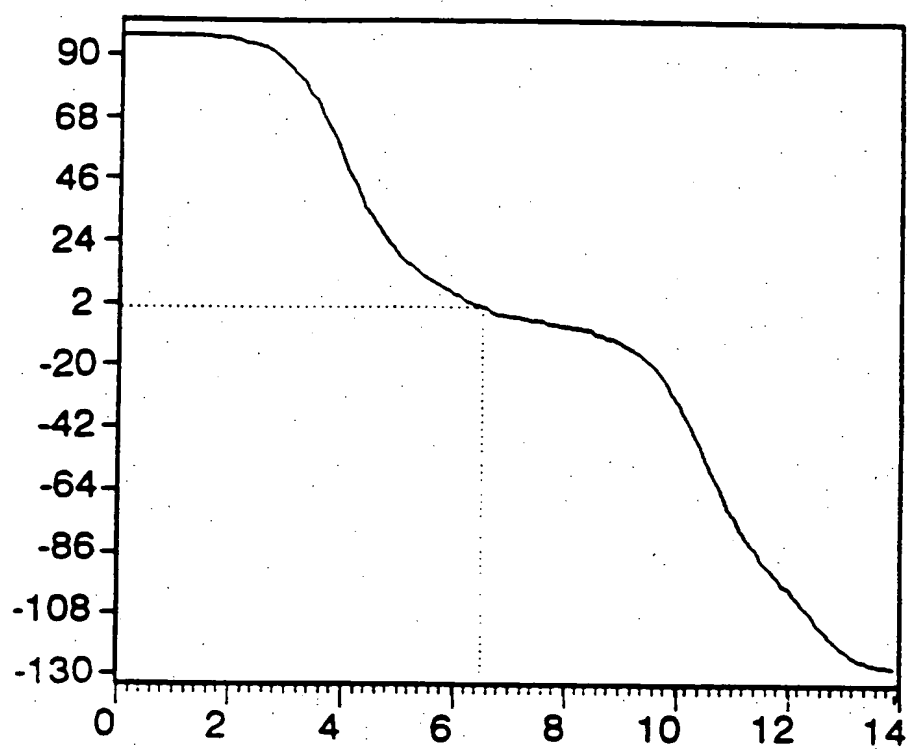


FIGURE 12B



13/130

FIGURE 13



17/130

FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X Extended conformation: -
 Turn conformation: > Coil conformation: *

10 20 30 40 50
 | | | | |
 MWNLLHETDSA V A T A R R P R W L C A G A L V L A G G F L L G F L F G W F I K S S N E A T

XXXXXXXXXXXXXXXXX--->>-----XXXXXXXXXXXXXXXXX
 XXXXXXXXXXXXXXXXXXXX--->>-----XXXXXXXXXXXXXXXXX

60 70 80 90 100
 | | | | |
 N I T P K H N M K A F L D E L K A E N I K K F L Y N F T Q I P H L A G T E Q N F Q L A K Q I Q S Q W

18/130

FIGURE 14-5

XXXXXXXXXXXXXXXXXX-->>-----*****XXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXX-->>-----*****XXXXXXXXXX-X*--

110 120 130 140 150
| | | | |
KEFGDVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEPPPG

-->>*****-->>-->>----->>***X----->>***>>
-->>*****-->>-->>----->>***X----->>***>>

160 170 180 190 200
| | | | |
YENVSDIVPPFSAFSPQGMPEGLVYVNVARTEDFFKLERDMKINCSGKI

21/130

FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX

-----XXXXXXXXXXXXXXXXX-X-----XXXXXXXX----->XXX

610 620 630 640 650

 | | | | |

AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFSERL

XXXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXXX

XXXXXXXXXXXXX-----X*XXXXXXXX-----XXXXXXXXXXXXXXXXXXXXX

660 670 680 690 700

 | | | | |

QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHHVIYAPSSHNKY

XX>>>*>-----XXXXXXXXXX-->>*>----->***>

XX>>>*>-----XXXXXXXXXX-->>*>----->***>

710 720 730 740 750

 | | | | |

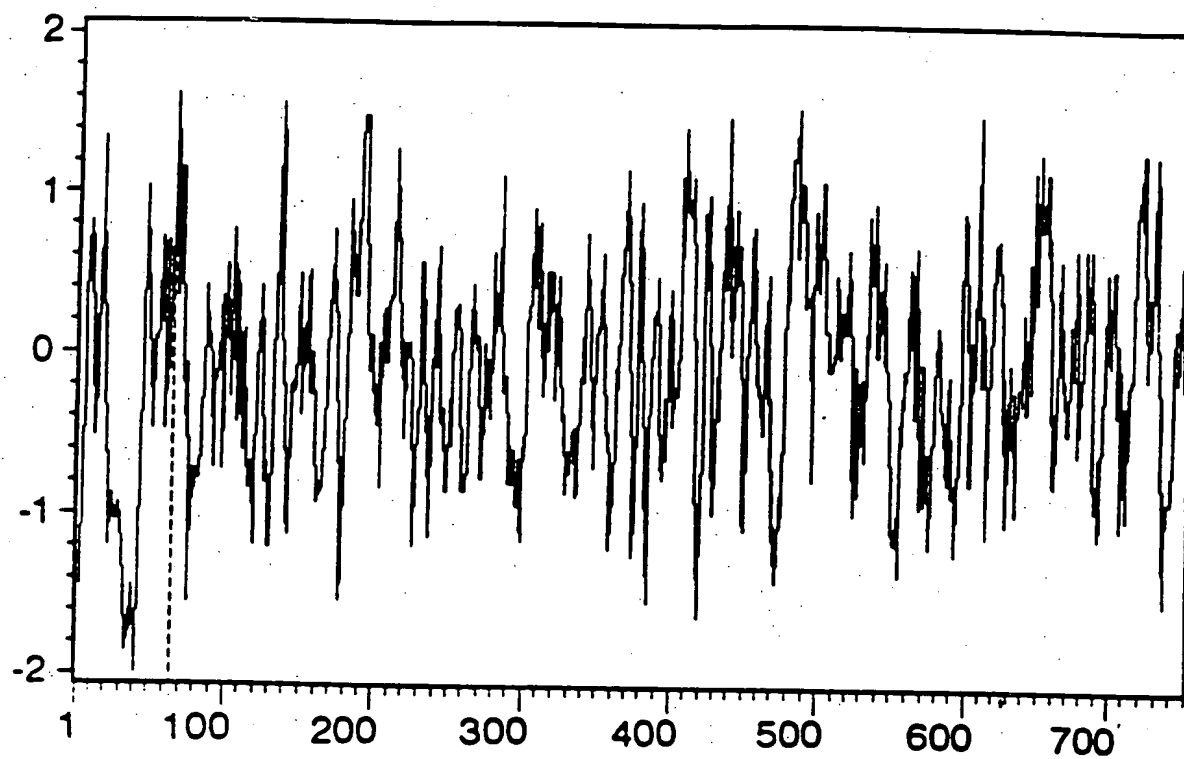
AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAETLSEVA

----->--XXXXXXXXXX**XXXXXXXXX-----XXXXXXXXXXXXXXXXXX

----->--XXXXXXXXXX**XXXXXXXXX-----XXXXXXXXXXXXXXXXXX

22/130

FIGURE 15A



23/130

FIGURE 15B

* * * * *
 * PREDICTION OF ANTIGENIC DETERMINANTS *
 * * * * *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1) Ah= 1.62 : From 63 to 68 : Asp-Glu-Leu-Lys-Ala-Glu
 (2) Ah= 1.57 : From 132 to 137 : Asn-Glu-Asp-Gly-Asn-Glu
 (3) Ah= 1.55 : From 482 to 487 : Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

FIGURE 16-1

The best scores are:

The best scores are:		initn	initl	opt
CHKTFER	G.gallus mRNA for transferrin receptor	203	120	321
RATTRFR	Rat transferrin receptor mRNA, 3' end.	164	164	311
HUMTFRR	Human transferrin receptor mRNA, complete cd	145	145	266

CHKTFER	G.gallus mRNA for transferrin receptor	203	120	321
51.9%	identity in 717 nt overlap			

1020	1030	1040	1050	1060	1070
pmsgen	TGTCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCCTCTCACACCAGGTTA				
			::: : ::::: ::: ::::: :		
CHKTFE	TACACTTATCCCATTCGGGACATGCCCCACCTTGGAACTGGAGACCCCTTACACCCCAGGCTT				
	990	1000	1010	1020	1030
					1040

```

1080      1090      1100      1110      1120      1130
pmsgen  CCCAGCAAATGAATATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT
        :::      :      :      :      :      :      :      :      :
CHKTFE  CCCTTCGTTCAACCAACCA---GTTTCCACCAGTTGAATCTTCAGGACTACCCACAT
        1050      1060      1070      1080      1090      1100

```

	1140	1150	1160	1170	1180	1190
pmsgen	TCCTGTTCA	TCCAAATTGGATA	TATGACAGAGCTCCTAGAAA	AATGGGTGGCTC		
	:	: : : : :	:	: : : :	:	: : : : :
CHKTFE	TGCTGTTCA	GACCATTCTTAGCAGTGCAGCAGCCAGGCTGTT	CAGCAAAA	AATGGATGGAGA		
	1110	1120	1130	1140	1150	1160

27/130

FIGURE 16-4

```

1680      1690      1700      1710      1720      1730
pmsgen  TACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC
        ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CHKTFE  TATATGCTGCTGGGAGTATTATGAAGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC
1630      1640      1650      1660      1670      1680

1740      1750      1760      1770      1780      1790
pmsgen  AAATCTCTTTATGAAGTTGGACTAAAAAAGTCCCTTCCCCAGAGTTCAGTGGCATGCCCC
        ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
CHKTFE  -----CTCTATAACAGACTTGGCCCCAGACTGGGTAAAGCAGTTGTTCTCTTGGCCTGGA
1690      1700      1710      1720      1730

```


FIGURE 16-8

pmsgen	GCTTTGAAGGCAAAATCTCTTAT-GAA-----AGTTGGACTAAAAAAGTCCTTCCCCCAG ::: :: : ::: :: : ::: :: : ::: :: :	1730	1740	1750	1760	1770
RATTRF	---TTGATGGAAAATACTATATCGAAACAGTAATTGGATTAGCAAATAATGAGGAACCTTT 1140 1150 1160 1170 1180 1190					
pmsgen	AGTTCAGTGGCATGCCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT	1780	1790	1800	1810	1820 1830
RATTRF	CCTTGGACAAATGCTGCATTCCCCTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTCT	1200	1210	1220	1230	1240 1250

FIGURE 16-9

HUMTFRR Human transferrin receptor mRNA, complete cd 145 145 266
54.3% identity in 464 nt overlap

	1230	1240	1250	1260	1270
pmsgen	AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC				
	:	:	:	:	:
HUMTFR	TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC				
1140	1150	1160	1170	1180	1190
1280	1290	1300	1310	1320	1330
pmsgen	AAAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAATTACAA				
:	:	:	:	:	:
HUMTFR	AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA				
1200	1210	1220	1230	1240	1250
1340	1350	1360	1370	1380	1390
pmsg n	TGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATCTCTGGGAGGTCA				
:	:	:	:	:	:
HUMTFR	CATCTTTGGAGTTATTAAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGCCCA				
1260	1270	1280	1290	1300	1310
1400	1410	1420	1430	1440	1450
pmsgen	CCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGT-GGAGCAGCTGTGTTCATG				
:	:	:	:	:	:
HUMTFR	GAGAGATGCATGGGGCCCTGGAGCTGC AAAATC-CGGTGTAGGCACAGCTCT'CCT'ATTGA				
1320	1330	1340	1350	1360	1370

34/130

FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCCAAATCTCTTTATG				
:	:	:	:	:	:
HUMTER	AAAACAATGCAGAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

35/130

FIGURE 17A

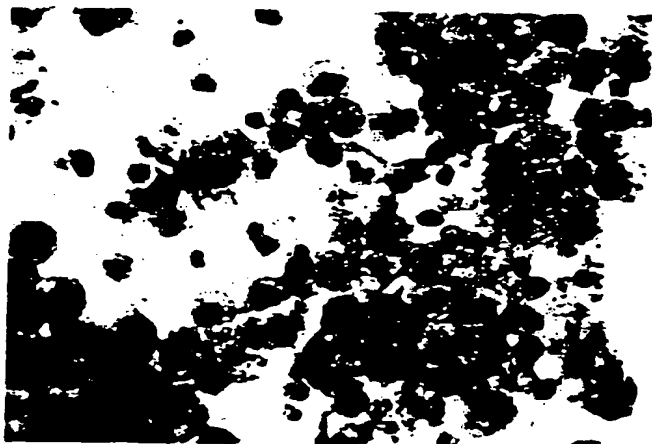


FIGURE 17B

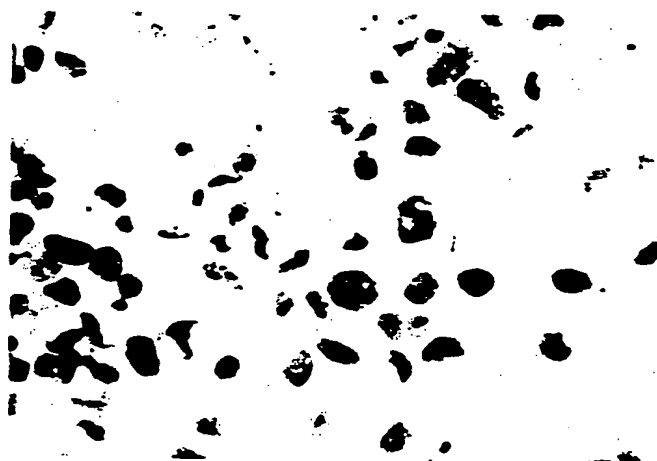
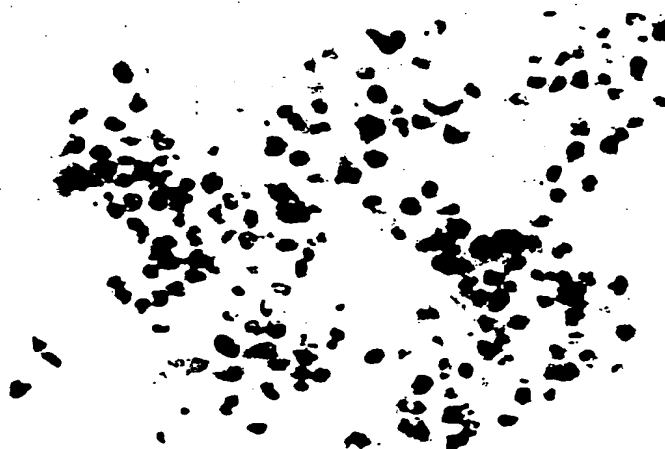
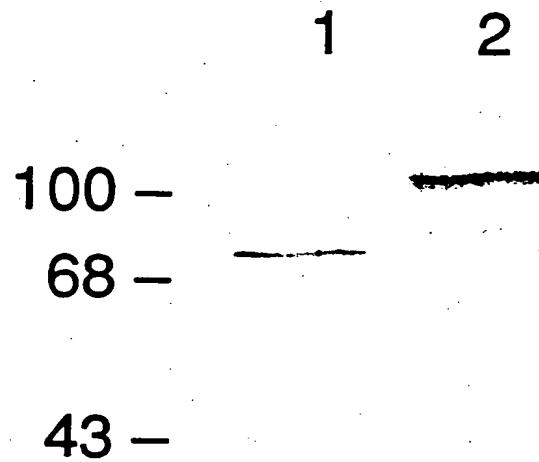


FIGURE 17C



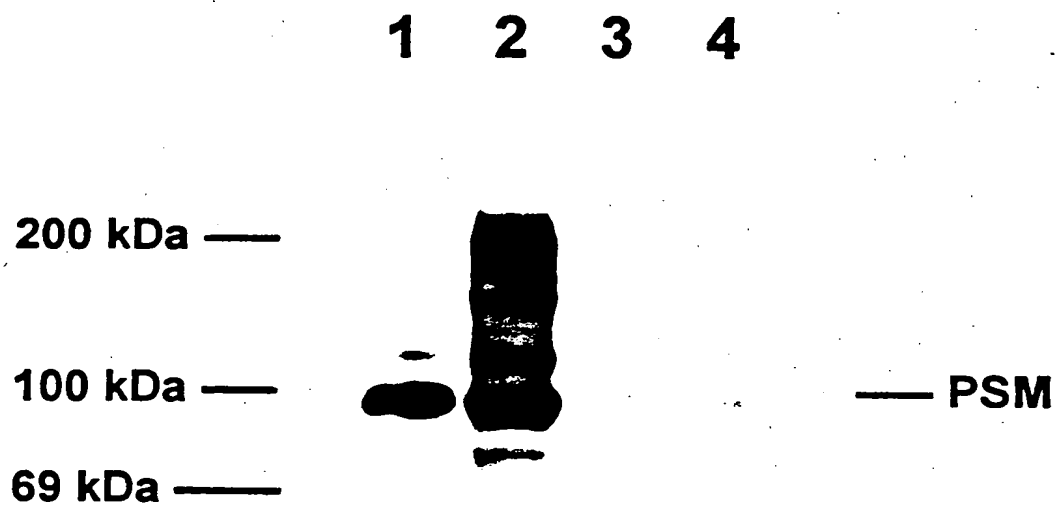
36/130

FIGURE 18



37/130

FIGURE 19



38/130

FIGURE 20

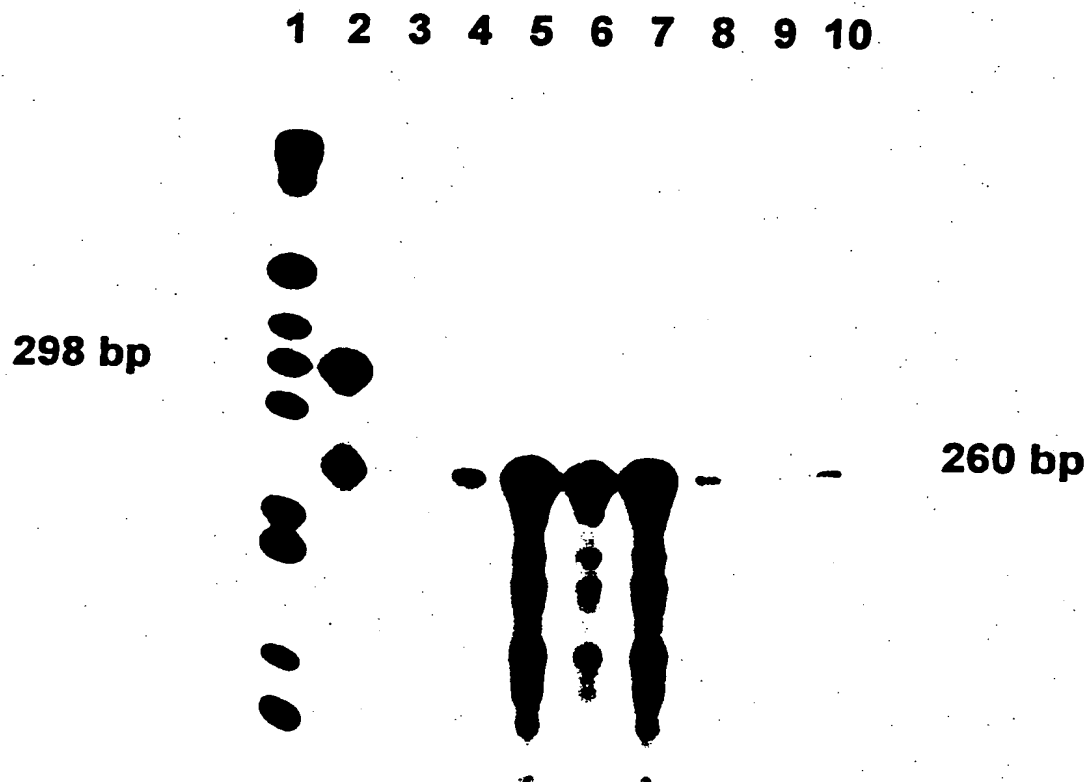
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

400

350

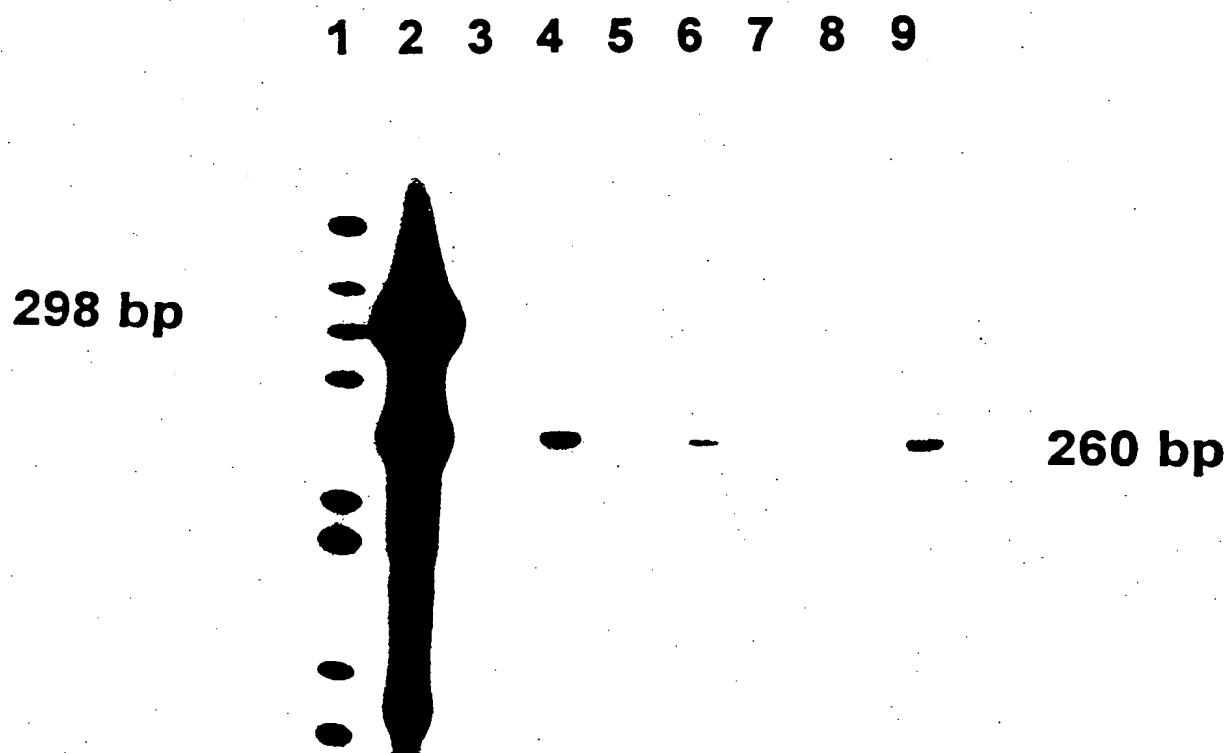
39/130

FIGURE 21



40/130

FIGURE 22



41/130
FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

42/130

FIGURE 24A

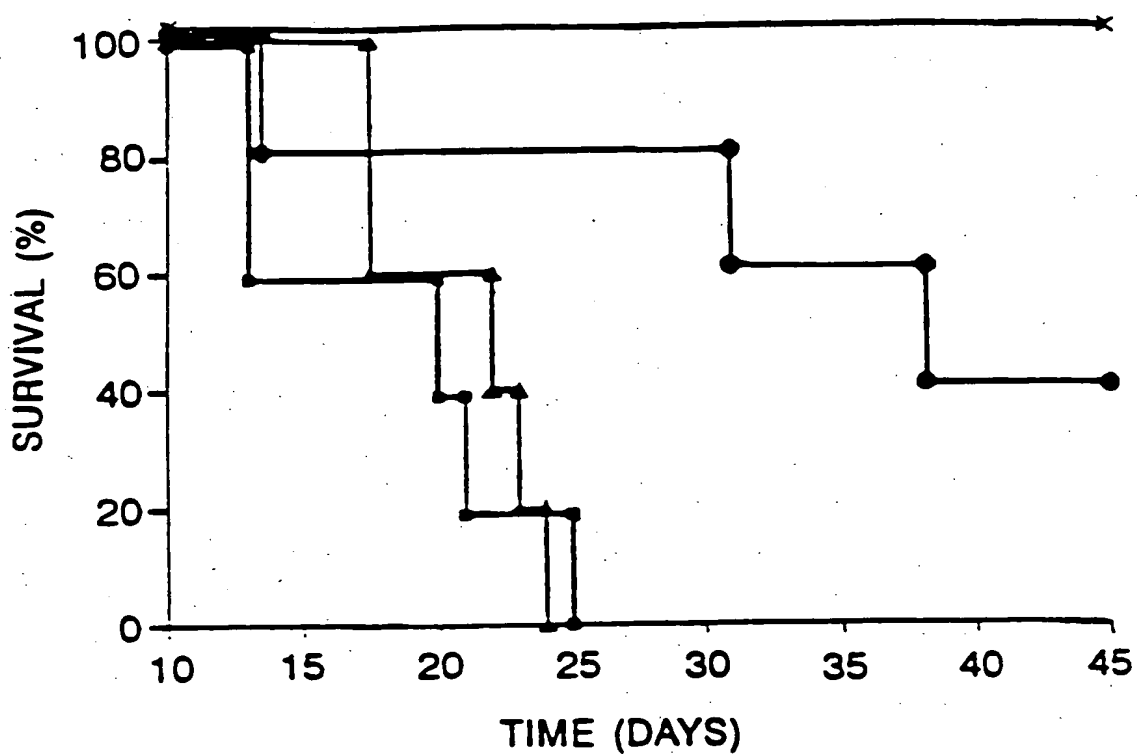
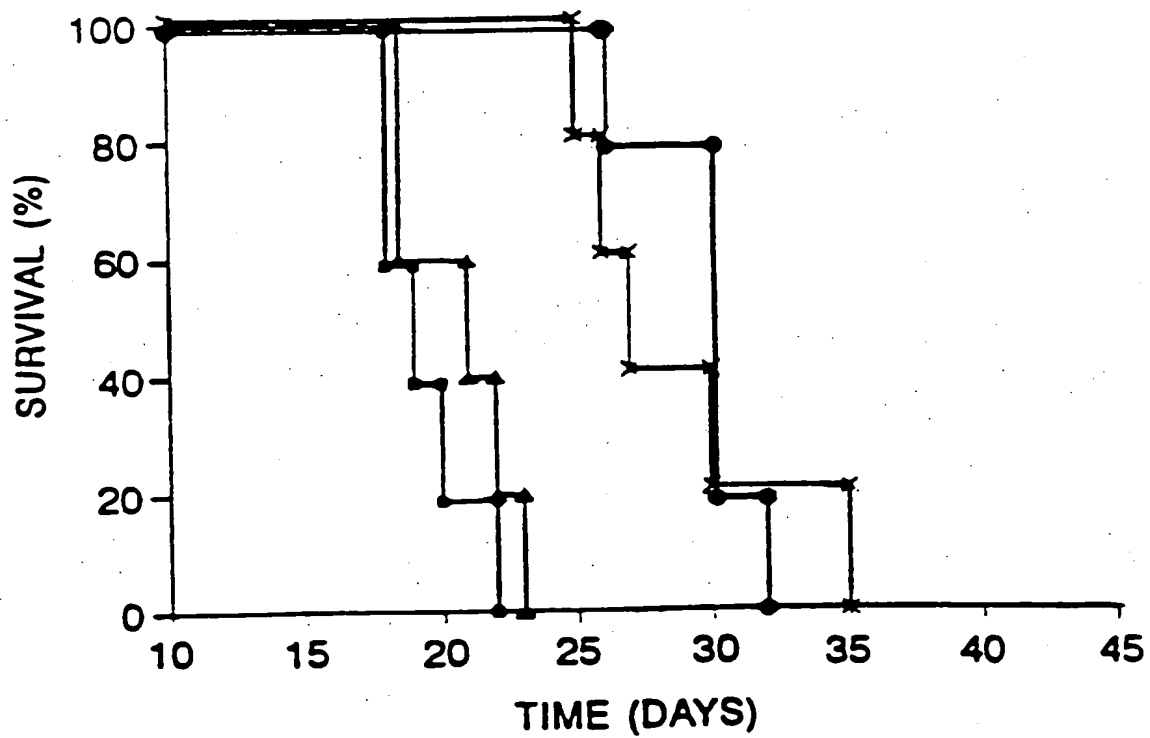


FIGURE 24B



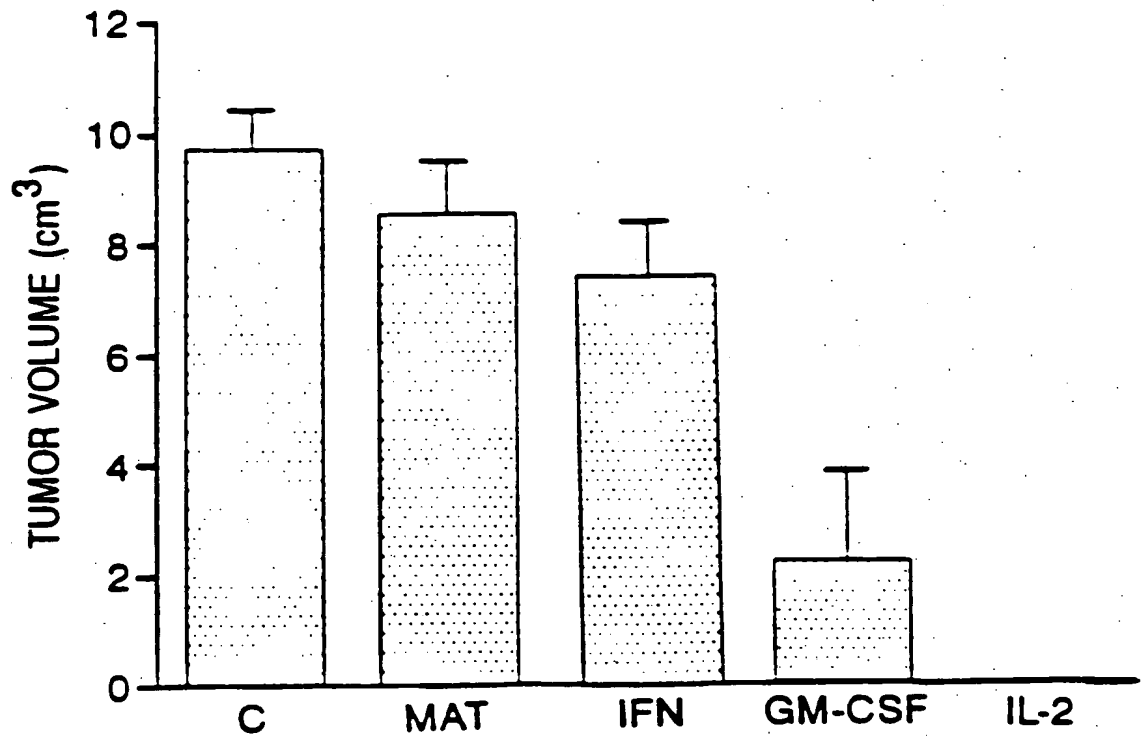
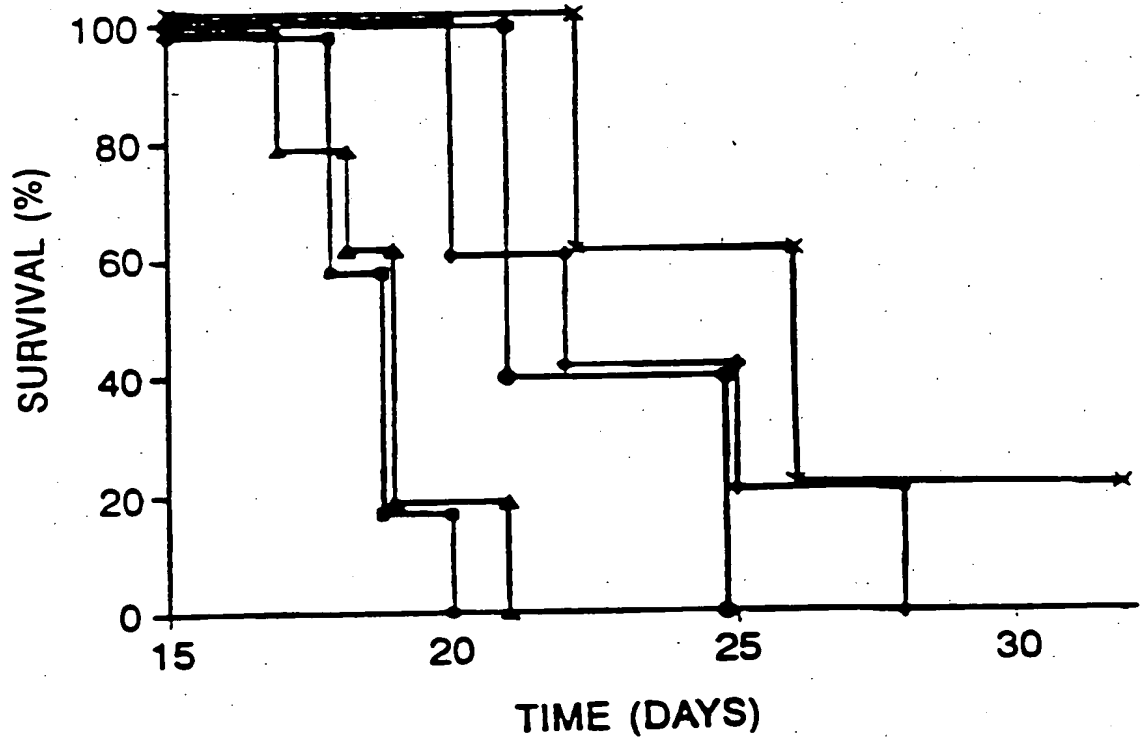
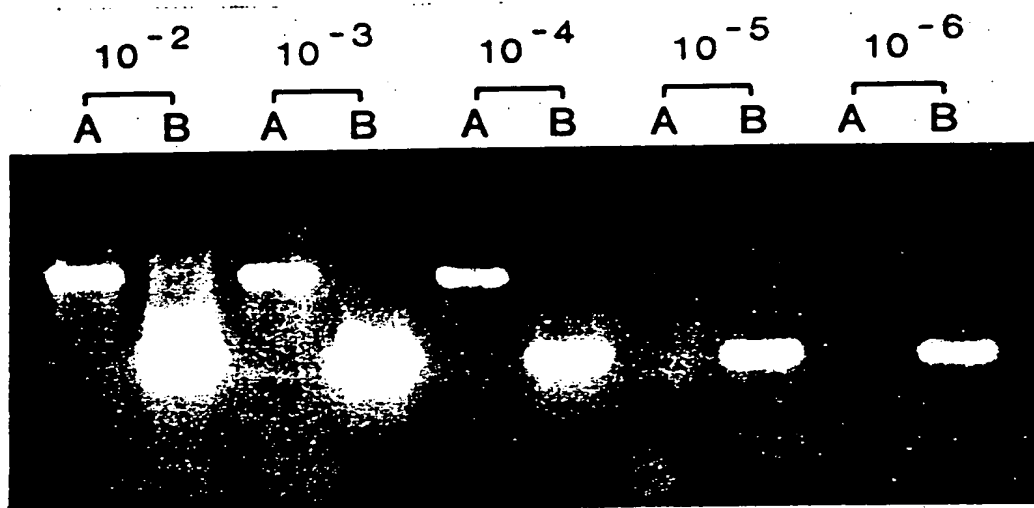
43/130
FIGURE 25A

FIGURE 25B



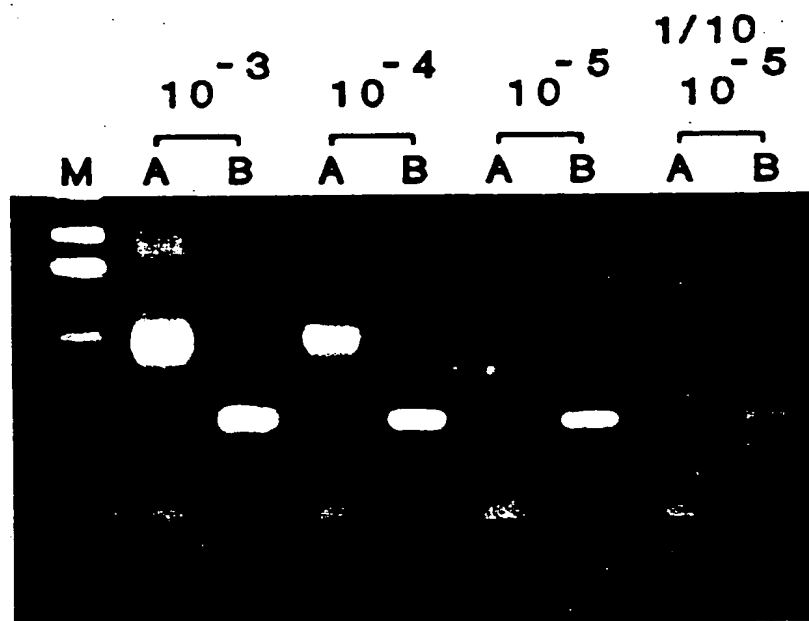
44/130

FIGURE 26



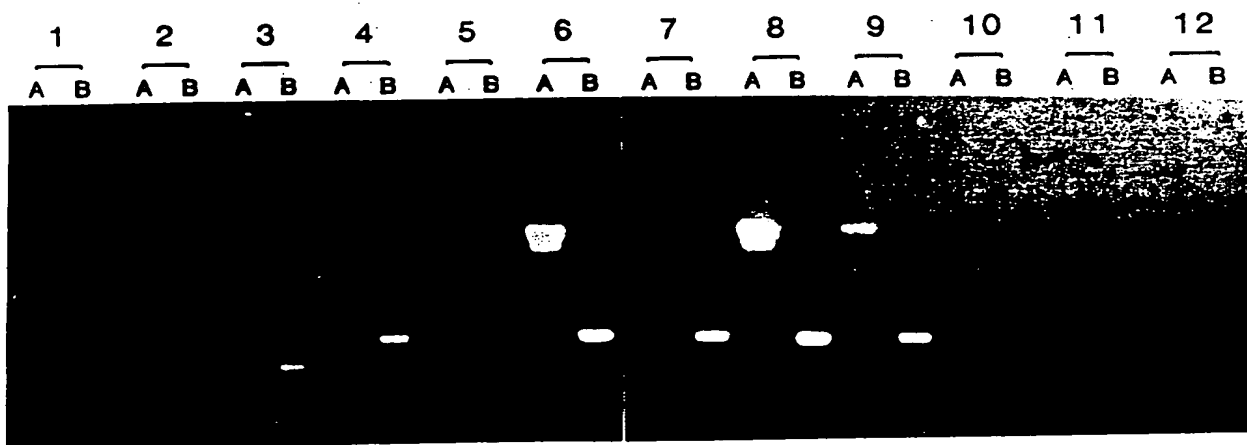
45/130

FIGURE 27



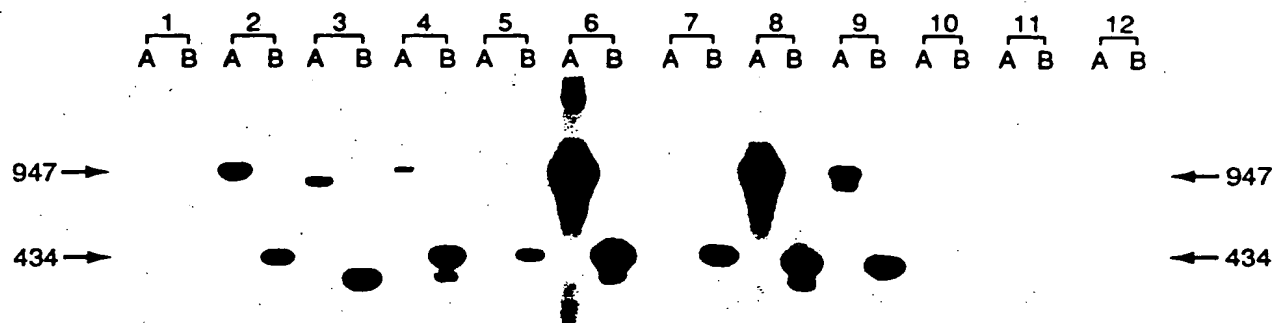
46/130

FIGURE 28



47/130

FIGURE 29



48/130

FIGURE 30

Patient	Stage	Tr atm nt	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

49/130

FIGURE 31A

	10	20	30	40	50	60
1	AAGGGTGCTC TTCCCACGAG	CTTAGGCTGA GAATCCGACT	ATGCTTGCAG TACGAACGTC	ACAGGATGCT TGTCTTACGA	TGGTTACAGA ACCAATGTCT	TGGGCTGTGA ACCCGACACT
61	CTCGAGTGGA GAGCTCACCT	GTTTTATAAG CAAAATATTC	GGTGCTCCTT CCACGAGGAA	AGGCTGAATG TCCGACTTAC	CTTGCAGACA GAACGTCTGT	GGATGCTTGG CCTACGAACC
121	TTACAGATGG AATGTCTACC	GCTGTGAGCT CGACACTCGA	GGGTGCTTGT CCCACGAACA	AAGAGGATGC TTCTCCTACG	TTGGGTGCTA AACCACGAT	AGTGAGCCAT TCACTCGGTA
181	TTGCAGTTGA AACGTCAACT	CCCTATTCTT GGGATAAGAA	GGAACATTCA CCTTGTAAGT	TTCCCCTCTA AAGGGGAGAT	CCCCTGTTTC GGGGACAAAG	TGTTCTGCCC ACAAGGACGG
241	AGCTAAGCCC TCGATTTCGG	ATTTTTTCATT TAAAAAGTAA	TTTCTTTTAA AAAGAAAATT	CTCCTTAGCG GAGGAATCGC	CTCCGCAAAA GAGGCGTTTT	CTTAATCAAT GAATTAGTTA
301	TTCTTTAAAC AAGAAATTTG	CTCAGTTTTTC GAGTCAAAAAG	TTATCTGTAA AATAGACATT	AAGGTAAATA TTCCATTTAT	ATAATACAGG TATTATGTCC	GTGCAACAGA CACGTTGTCT
361	AAAATCTAGT TTTTAGATCA	GTGGTTTACA CACCAAATGT	TAATCAGCTG ATTAGTGGAC	TTAGAGATTT AATCTCTAAA	TAAATTATTT ATTTAATAAA	CAGGATAAGT GTCCTATTCA
421	CATGATAATT GTACTATTAA	AAATGAAATA TTTACTTTAT	ATGCACATAA TACGTGTATT	AGCACATAGT TCGTGTATCA	GTGGTGTCCT CACCACAGGA	CCATATAGAA GGTATATCTT
481	AATGCTCAGT TTACGAGTCA	ATATTGGTTA TATAACCAAT	TTAACTACTT AATTGATGAA	GTTGAAGGTT CAACTTCCAA	TATCTTCTCC ATAGAAGAGG	ACTAAACTGT TGATTTGACA
541	AAGTTCCACA TTCAAGGTGT	AGCCTTACAA TCGGAATGTT	TATGTGACAG ATACACTGTC	ATATTCATTC TATAAGTAAG	ATTGTCTGAA TAACAGACTT	TTCTTCAAAT AAGAAGTTTA
601	ACATCCTCTT TGTAGGAGAA	CACCATAGCG GTGGTATCGC	TCTTATTAAT AGAATAATTA	TGAATTATTA ACTTAATAAT	ATTGAATAAA TAACTTATTT	TTCTATTGTT AAGATAACAA
661	CAAAAATCAC GTTTTTAGTG	TTTTATATTT AAAATATAAA	AACTGAAATT TTGACTTTAA	TGCTTACTTA ACGAATGAAT	TAATCACATC ATTAGTGTAG	TAACCTTCAA ATTGGAAGTT
721	AGAAAACACA TCTTTTGTGT	TTAACCCTT AATTGGTTGA	GTAAGGGGTA CATGACCCAT	ATGTTACTGG TACAATGACC	GTGATCCAC CACTAGGGTG	GTTTTACAAA CAAAATGTTT

50/130

FIGURE 31B

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781 TGAGAAGATA TATTCTGGTA AGTTGAATAC TTAGCACCCA GGGGTAATCA GCTTGGACAG
    ACTCTTCTAT ATAAGACCAT TCAACTTATG AATCGTGGGT CCCCATTAGT CGAACCTGTC

841 GACCAGGTCC AAAGACTGTT AAGAGTCTTC TGA CTCCAAA CTCAGTGCTC CCTCCAGTGC
    CTGGTCCAGG TTTCTGACAA TTCTCAGAAG ACTGAGGTTT GAGTCACGAG GGAGGTCACG

901 CACAAGCAAA CTCCATAAAG GTATCCTGTG CTGAATAGAG ACTGTAGAGT GGTACAAAGT
    GTGTTCGTTT GAGGTATTTC CATAGGACAC GACTTATCTC TGACATCTCA CCATGTTTCA

961 AAGACAGACA TTATATTAAG TCTTAGCTTT GTGACTTCGA ATGACTTACC TAATCTAGCT
    TTCTGTCTGT AATATAATTC AGAATCGAAA CACTGAAGCT TACTGAATGG ATTAGATCGA

1021 AAATTTTCAGT TTTACCATGT GTAAATCAGG AAGAGTAATA GAACAAACCT TGAAGGGTCC
    TTTAAAGTCA AAATGGTACA CATTTAGTCC TTCTCATTAT CTTGTTTGGA ACTTCCCAGG

1081 CAATGGTGAT TAAATGAGGT GATGTACATA ACATGCATCA CTCATAATAA GTGCTCTTTA
    GTTACCACTA ATTTACTCCA CTACATGTAT TGTACGTAGT GAGTATTATT CACGAGAAAT

1141 AATATTAGTC ACTATTATTA GCCATCTCTG ATTAGATTTG ACAATAGGAA CATTAGGAAA
    TTATAATCAG TGATAATAAT CGGTAGAGAC TAATCTAAAC TGTTATCCTT GTAATCCTTT

1201 GATATAGTAC ATTCAGGATT TTGTTAGAAA GAGATGAAGA AATTCCCTTC CTTCTGCCC
    CTATATCATG TAAGTCCTAA AACAACTCTT CTCTACTTCT TTAAGGGAAG GAAGGACGGG

1261 TAGGTCATCT AGGAGTTGTC ATGGTTCATT GTTGACAAAT TAATTTTCCC AAATTTTTC
    ATCCASTAGA TCCTCAACAG TACCAAGTAA CAACTGTTTA ATTAAGGAGG TTTAAAAAGT

1321 CTTTGCTCAG AAAGTCTACA TCGAAGCACC CAAGACTGTA CAATCTAGTC CATCTTTTTC
    GAAACGAGTC TTTGAGATGT AGCTTCGTGG GTTCTGACAT GTTAGATCAG GTAGAAAAAG

1381 CACTTAACTC ATACTGTGCT CTCCCTTTCT CAAAGCAAAC TGTTTGCTAT TCCTTGAATA
    GTGAATTGAG TATGACACGA GAGGGAAAGA GTTTCGTTTG ACAAACGATA AGGAACTTAT

1441 CACTCTGAGT TTTCTGCCTT TGCCTACTCA GCTGGCCCAT GGCCCTAAT GTTCTTCTC
    GTGAGACTCA AAAGACGGAA ACGGATGAGT CGACCGGGTA CCGGGGATTA CAAAGAAGAG

1501 ATCTCCACTG GGTCAAATCC TACCTGTACC TTATGGTTCT GTTAAAGCA GTGCTTCCAT
    TAGAGGTGAC CCAGTTTAGG ATGGACATGG AATACCAAGA CAATTTTCGT CACGAAGGTA

1561 AAAGTACTCC TAGCAAATGC ACGGCCTCTC TCACGGATTA TAAGAACACA GTTTATTTTA

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51/130

FIGURE 31C

```

TTTCATGAGG ATCGTTTACG TGCCGGAGAG AGTGCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
      ATTTTCGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
      CCCTATATTA AAACATACTA CTAAGAAGAC CAATTAGGTT GGTTCCTAACT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TGCCTTCAAC
      TAATGCATTC TGTCAATCGGT CTGTATCGGC CCTATACTTT TATTTTCAGAG ACGGAAGTTG

1801 AAGTTCCAGT ATTCTTTTCT TTCCTCCCCT CCCCTCCCCT CCCTTCCCCT CCCCTTCCTT
      TTCAAGGTCA TAAGAAAAGA AAGGAGGGGA GGGGAGGGGA GGAAGGGGA GGGGAAGGAA

1861 CCCTTTCCCT TCCCTTCCTT TCTTTCTTGA GGGAGTCTCA CTCTGTCACC AGGCTCCAGT
      GGGAAAGGGA AGGGAAGGAA AGAAAGAAGT CCCTCAGAGT GAGACAGTGG TCCGAGGTCA

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCCGCCTCCC CGGTTCAAGC GATTCTCCTG
      CGTCACCGCG ATAGAACCGA CTGACGTTGG AGGCGGAGGG GCCAAGTTCC CTAAGAGGAC

1981 CCTCAGCCTC CTGAGTAGCT GGGACTACAG GAGCCCGCCA CCACGCCAG CTAATTTTGT
      GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTGCGGGTC GATTAAAAAC

2041 TATTTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
      ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
      GCACTAGGCG GACAGACCCG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGCGG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAT
      CCCGAAATTT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

2221 AACATAAATA TTCTTTAGGA AAAAGGGCGC GGTGGTGATT TACACTGATG ACAAGCATTC
      TTGTTATTAT AAGAAATCCT TTTTCCCGCG CCACCACTAA ATGTGACTAC TGTTTCGTAAG

2281 CCGACTATGG AAAAAAAGCG CAGCTTTTTT TGCTCTGCTT TTATTCAGTA GAGTATTGTA
      GGCTGATACC TTTTTTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

2341 GAGATTGTAT AGAATTTTCAG AGTTGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
      CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

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52/130

FIGURE 31D

2401 GGAGAGTCTC TTTCTTCCTT TCATTTTAT ATTTAAGCAA GAGCTGGACA TTTTCCAAGA
CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCGTT CTCGACCTGT AAAAGGTTCT

2461 AAGTTTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCCGGA TTTCTTCTC CTGGAGGCAG
TTCAAAAAAA AAAAATTCCG CGGAGAGTTT TCCCCGGCCT AAAGGAAGAG GACCTCCGTC

2521 ATGTTGCCTC TCTCTCTCGC TCGGATTGGT TCAGTGCACT CTAGAAACAC TGCTGTGGTG
TACAACGGAG AGAGAGAGCG AGCCTAACCA AGTCACGTGA GATCTTTGTG ACGACACCAC

2581 GAGAAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTCGGACG TCCCGACTAT TCGCTCCGTA

2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGGTTG GAGGGCGCGC AGTAGAGCAG
ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCGTC

2701 CAGCACAGGC GCGGGTCCCG GGAGGCCGGC TCTGCTCGCG CCGAGATGTG GAATCTCCTT
GTCGTGTCCG CGCCCAGGGC CCTCCGGCCG AAGCGAGCGC GGCTCTACAC CTTAGAGGAA

2761 CACGAAACCG ACTCGGCTGT GGCCACCGCG CGCCGCCCCG GCTGGCTGTG CGCTGGGGCG
GTGCTTTGGC TGAGCCGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

2821 CTGGTGCTGG CGGGTGGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GCGCCTCGC
GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGGAGCG

2881 GGAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTCAGCTGC
CCTCGTTTGG AGCCTCAGAA GGGGCACCAC GCGGCCACGA CCCTGAGCGC CCAGTCGACG

2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCCA GGGGCGGCGA TTAGGGTCGG GGTAATGTGG
GCTCACCTA GGACAACGAC CAGAAGGGGT CCCC GCCGCT AATCCCAGCC CCATTACACC

3001 GGTGAGCACC CCTCGAG
CCACTCGTGG GGAGCTC

53/130

FIGURE 32

Potential binding sites on the PSM promoter*

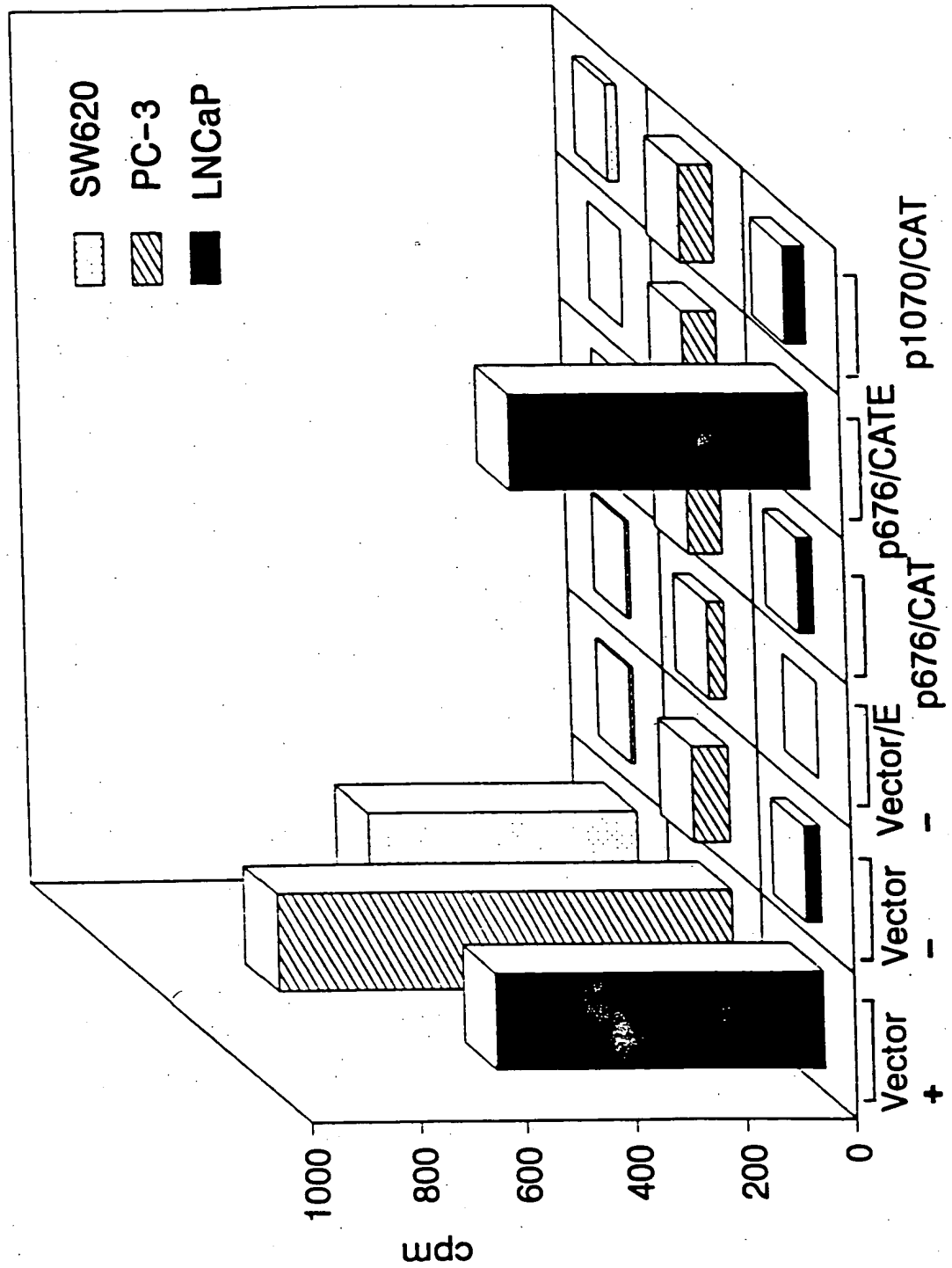
Site	Seq	**Location	#nt matched
AP1	TKAGTCA	1145	7/7
E2-RS	ACCNNNNNNGGT	1940	12/12
		1951	12/12
GHF	NNNTAAATNNN	580	11/11
		753	11/11
		1340	11/11
		1882	11/11
		1930	11/11
		1979	11/11
		2001	11/11
		2334	11/11
		2374	11/11
		2591	11/11
		2620	11/11
		2686	11/11
JVC repeat	GGGNGGRR	1155	8/8
		1175	8/8
		1180	8/8
		1185	8/8
		1190	8/8
NFkB	GGGRHTYYHC	961	10/10
uteroglobi	RYYWSGTG	250	8/8
		921	8/8
		1104	8/8

IFN AAWAANGAAAGGR590 13/13 Cell 41:509 (1985)

* the PSM promoter sequence 683XFRVS (Fig. 1) starts from the 5' end of the promoter fragment. The 3' region overlaps the previously published PSM cDNA at nt#2485, i.e. the putative transcription start site is at nt#2485 on sequence 683XFRVS. **The number referred to in this table is in reference to sequence 683XF107 which is the complement and inverse of 683XFRVS.

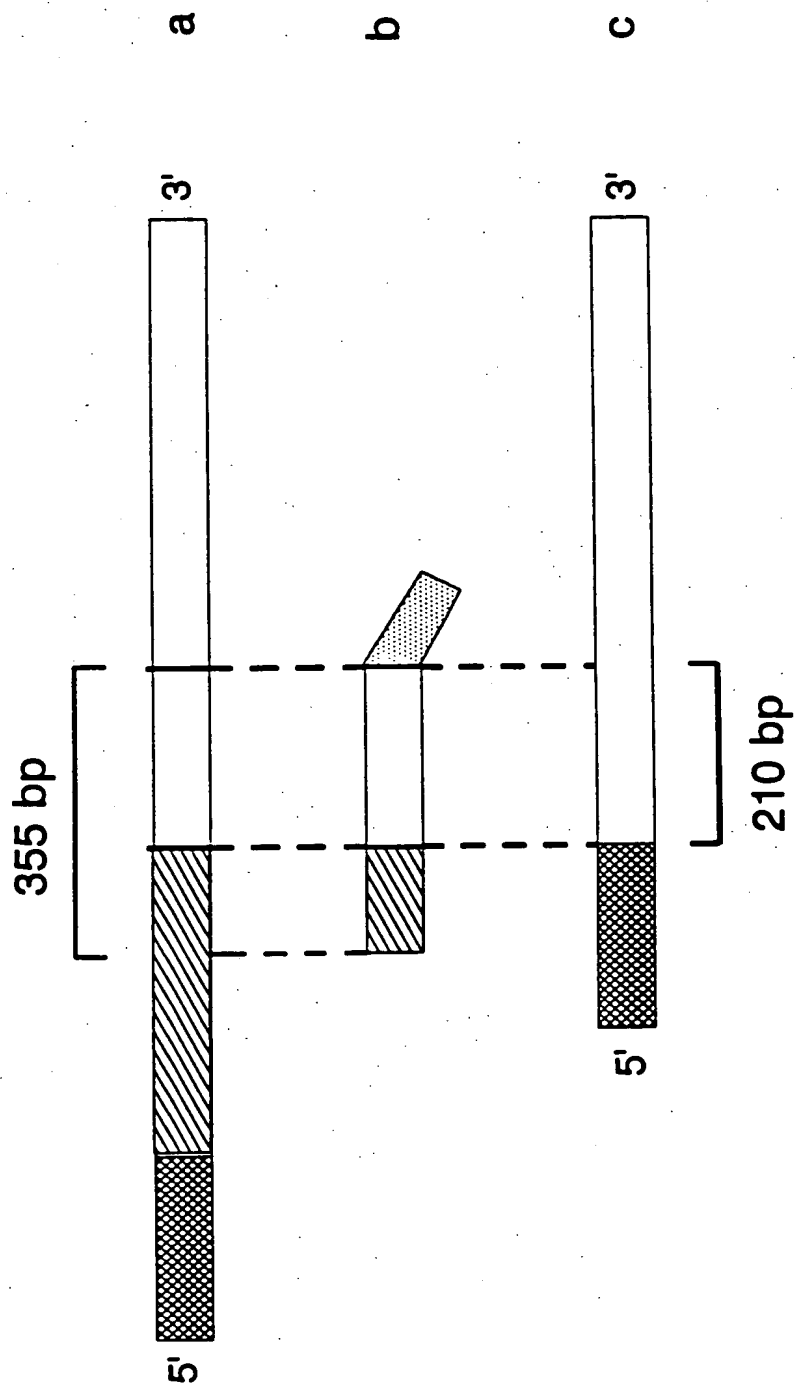
54/130

FIGURE 33



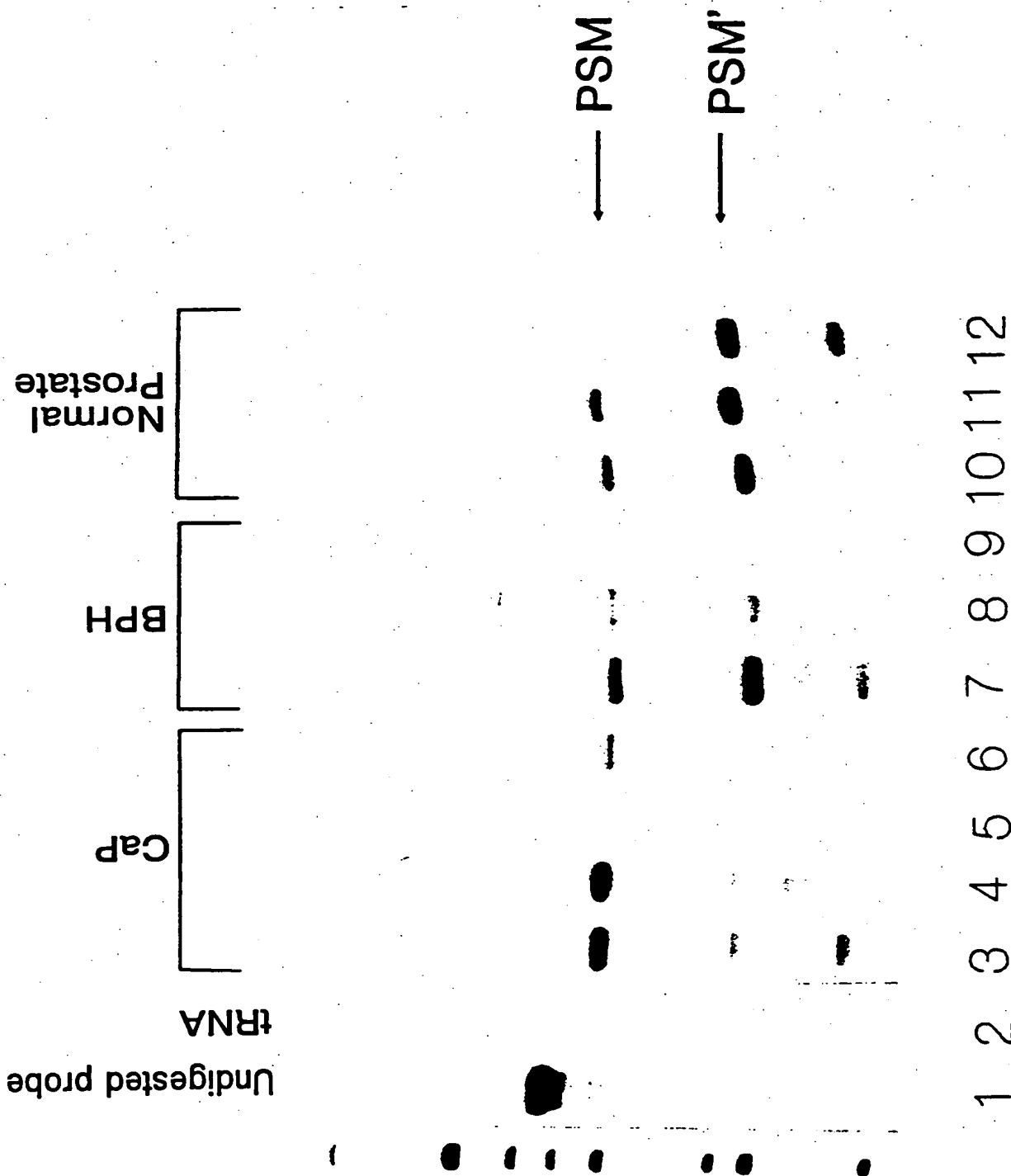
56/130

FIGURE 35



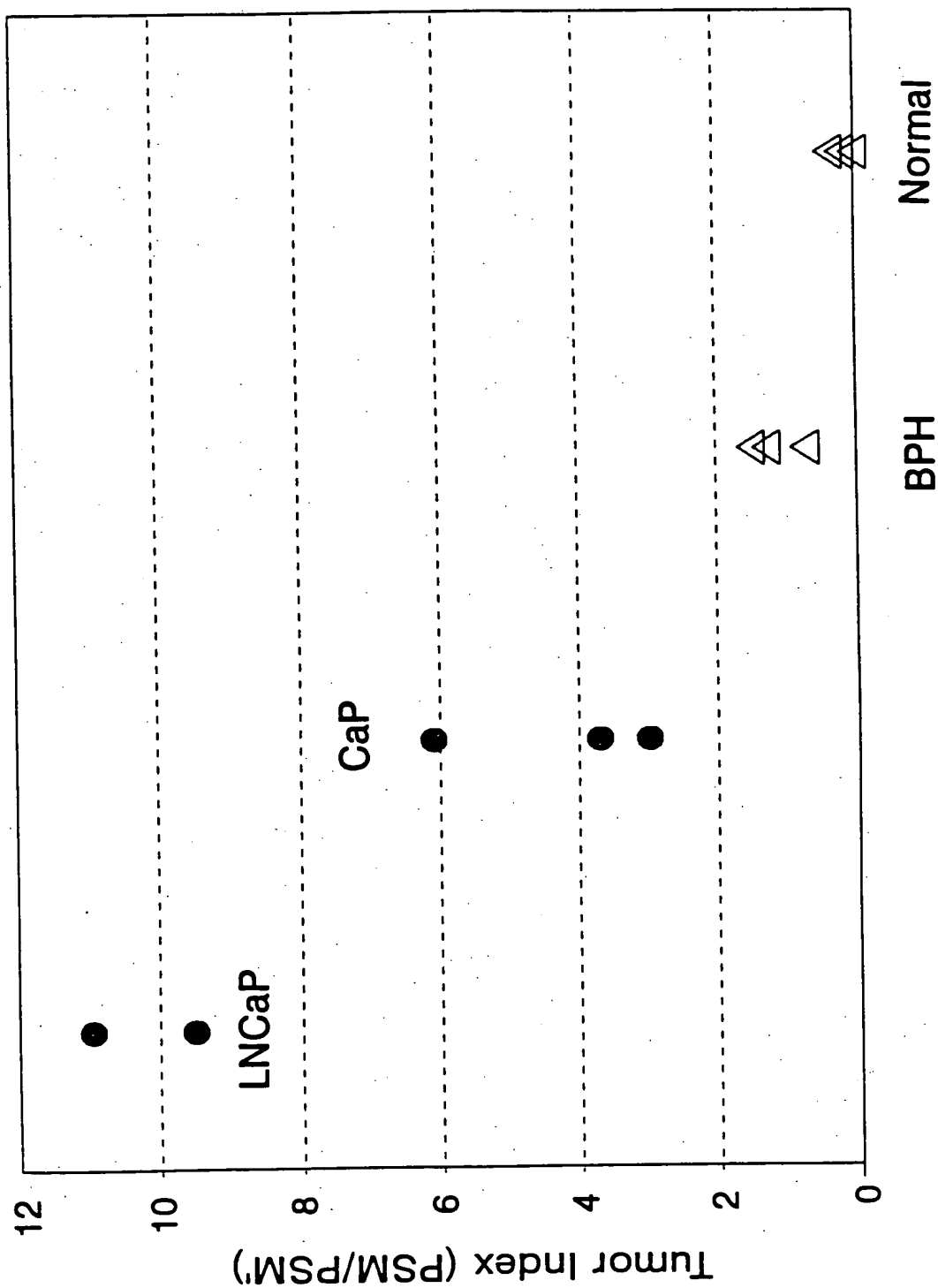
57/130

FIGURE 36



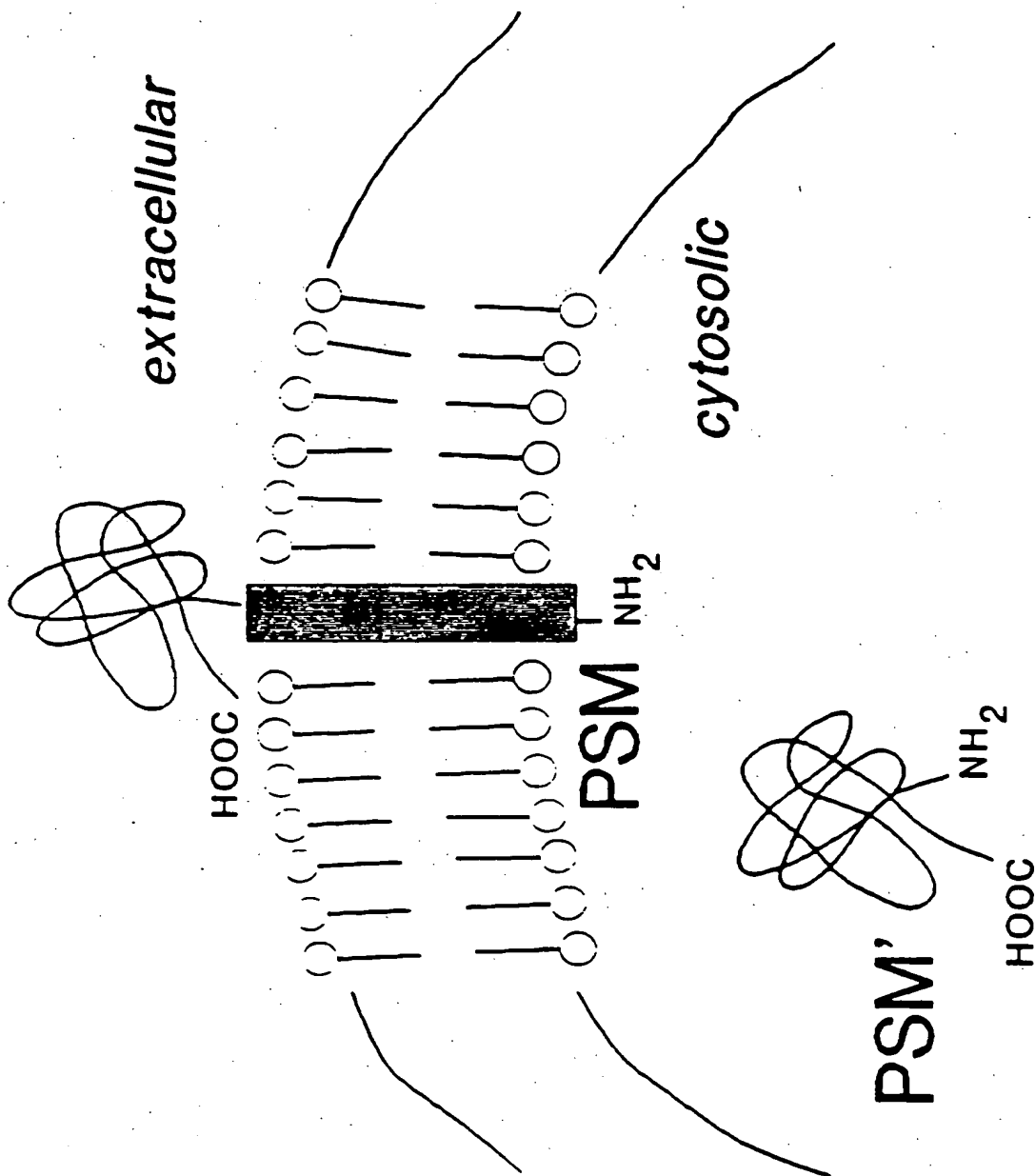
58/130

FIGURE 37



59/130

FIGURE 38



60/130

FIGURE 39

	10	20	30	40	50	60
1	TTTGCAGACT AAACGTCTGA	TGACCAACTT ACTGGTTGAA	TCTAAGAAAA AGATTCTTTT	GCAGAACCAC CGTCTTGGTG	ACAGGCAAGC TGTCCGTTTC	TCAGACTCTT AGTCTGASAA
61	TTATTAAATT AATAATTTAA	CCAGTTTTGA GGTCAAACT	CTTTGCCACT GAAACGGTGA	TCTTAGTGGC AGAATCACCG	CTTGAACAAG GAACTTGTTT	TTACCGAGTC AATGGCTCAG
121	CTCTCAGCGT GAGAGTCGCA	TAGTTACCCT ATCAATGGGA	ATTTTAATGA TAAAATTACT	TGAGGATAAT ACTCCTATTA	ATTATCTGCC TAATAGACGG	CAAATTATTG GTTTAATAAC
181	GTATAGTAAA CATATCATTT	TATATAGCAT ATATATCGTA	GTAAATCTCC CATTTAGAGG	TAGCAGAGTA ATCGTCTCAT	CTGGGATTTT GACCCTAAAG	GCCACTTTAT CGGTGAAATA
241	TTCTTCTTTA AAGAAGAAAT	CCAAGATACT GGTTCTATGA	CCTATTGGAC GSATAACCTG	TTAATACACA AATTATGTGT	GGACTAGTCT CCTGATCAGA	AAGGTATCAC TTCCATAGTG
301	CAGGTAGTCC GTCCATCAGG	ACTCCTGCTC TGAGGACGAG	GGAATCTGAC CCTTAGACTG	CCGGGATTAG GGCCCTAATC	AGTAGGGCAT TCATCCCGTA	GGACCAGATG CCTGGTCTAC
361	GGTTTAAACA CCAAATTTGT	AATTCAATAT TTAAGTTATA	CTTCCACTAG GAAGGTGATC	CTTCACCTTG GAAGTGGAAC	GGGTTGTAAA CCCAACATTT	AGTTTTTTGAA TCAAAAACCTT
421	CCACACACTG GGTGTGTGAC	TGCTCATAAC ACGAGTATTG	AATCTTCATC TTAGAAGTAG	TCTTAAAAGG AGAATTTTCC	ATTTTATTCT TAAAATAAGA	TCCTGGTATC AGGACCATAG
481	CTCACTCTCA GAGTGAGAGT	TCCCTTGAT AGGGAACATA	TCCGTGCTCA AGGCACGAGT	GTGGCTGACA CACCGACTGT	CAGAAGAGTT GTCTTCTCAA	CTTTATNNNN GAAATANNNN
541	NNNNNNNNNN NNNNNNNNNN	CATCCTGTTT GTAGGACAAG	ATTTTTTCAGA TAAAAAGTCT	TCTCAGTTCA AGAGTCAAGT	AGCATCTCGT TCGTAGAGCA	CCTCAGTGTG GGAGTCACAC
601	GTGTTNNCTG CACAANNGAC	ATCCCTCACT TAGGGAGTGA	CTAATCCAAG GATTAGGTTT	TCTTTCTGTT AGAAAGACAA	TTATGCACAG AATACGTGTC	GTTGGAATCT CAACCTTAGA
661	TATTTCCGTT ATAAAGGCAA	TGCGNNCCAA ACGCNNGGTT	TCNAATNGTA AGNTTANCAT	TTAATATGC AAATTATACG	ATGTATATAT TACATATATA	GTATGTGCAT CATACACGTA
721	TTGTATGCTA AACATACGAT	NGCGATTAAG NCGCTAATTC	AACTAGAATA TTGATCTTAT	ATTAATAATT TAATTATTAA	GGAAGTCTAG CCTTCAGATC	AAGTGG TTCACC

61/130

FIGURE 40A

	10	20	30	40	50	60
1	TGAAAAATAC ACTTTTTATG	ATCAAAAATA TAGTTTTTAT	GGCATGAGAT CCGTA CTCTA	ACGAGCCTAT TGCTCGGATA	AGATAGGACT TCTATCCTGA	TATTTTTTAT ATAAAAAATA
61	TATTGTTGTA ATAACAACAT	TGTATTATTT ACATAATAAA	GTAAACACA CATTTTGTGT	AATTATCAAT TTAATAGTTA	ATTACCTCTG TAATGGAGAC	ACATTAGGTG TGTAATCCAC
121	AGATATTCTG TCTATAAGAC	AATTTTAATT TTAAAATTAA	TCTCTTGCC AGAGAACGGA	ACTTTCAC TG TGAAAGTGAC	AAAAAGAGTC TTTTTCTCAG	ATGCAAAACA TACGTTTGTC
181	ATTTTAAAGT TAAAAATTCA	TGCAAACCAA ACGTTTG GTT	TTGCAAAATA AACGTTT TAT	TTTTTTTATC AAAAAAATAG	CAACTTCAAT GTTGAAGTTA	GATAGGTATT CTATCCATAA
241	GCTGTTAATT CGACAATTAA	CTAAGATATG GATTCTATAC	CATTAATTGT GTAATTAACA	TTCAACTAAT AAGTTGATTA	GGGTGTCAAA CCCACAGTTT	CGAGATGTTT GCTCTACAAG
301	TGAAAATGAA ACTTTTACTT	GGCAAAAAGG CCGTTTTTCC	AGATCCACCT TCTAGGTGGA	TCTACTTTCA AGATGAAAGT	TAAAGTTTCT ATTTCAAAGA	ATCTTCCTCT TAGAAGGAGA
361	GCTGACTCAA CGACTGAGTT	ATAAGCATT TATTCSTAAA	AATACATTTT TTATGTAAAA	ATAACGAATT TATTGCTTAA	AATTATGAAT TTAATACTTA	ATATTTCAAA TATAAAGTTT
421	TAAATAAATT ATTTATTTAA	ATTTCCAAGT TAAAGGTTCA	GTTGAASGAA CAACTTCCTT	ATTCAGACTT TAAGTCTGAA	CTAATTTGCT GATTAAACGA	CTGATTCTGA GACTAAGACT
481	AACTAAAACA TTGATTTTGT	AATGCTCTGT TTACGAGACA	GAGAGTTTGC CTCTCAAACG	GTTTCCAGTG CAAAGGTCAC	AATAGCGGTG TTCATCGCAC	AGAAATCCAA TCTTTAGGTT
541	GTCAGACAGC CAGTCTGTCTG	TACATGAAAC ATGTACTTTG	TACATTTACC ATGTAAATGG	AGCTCTCTGC TCGAGAGACG	CAGACACCAG GTCTGTGGTC	TGCACGATAG ACGTGCTATC
601	CGCAGAACAT GCGTCTTGTA	GTAGCTAGAT CATCGATCTA	CTCAGTCATA GAGTCAGTAT	GCTNNNNNNN CGANNNNNNN	NNNNNNNNNN NNNNNNNNNN	AGACCTTGCA TCTGGAACGT
661	GTTGGCTTTT CAACCGAAAA	AACCTGAAGG TTGGACTTCC	AGATAAGGCA TCTATTCCGT	AGATTCCAGG TCTAAGGTCC	GTTTATTTAG CAAATAAATC	AGAAATTACA TCTTTAATGT
721	GGATCTGGGA CCTAGACCCT	ATAAAGTAGT TATTTTCATCA	TACAAAATTA ATGTTTTTAAT	GTCCCCAACC CAGGGGTTGG	AGCTTTCATG TCGAAAGTAC	GAGCTTTTCAA CTCGAAAGTT

62/130

FIGURE 40B

781 TTATTAATTA TTCTAGTTCT TAATCGCATG CATACAATGC ACATACATAT ATACATGCAT
AATAATTAAT AAGATCAAGA ATTAGCGTAC GTATGTTACG TGTATGTATA TATGTACGTA

841 ATTAAAATAC ATGATTGGAC GCAAACGGAA ATAAGATTCC ACCTGTGCAT AAAACAGAA
TAATTTTATG TACTAACCTG CGTTTGCCTT TATTCTAAGG TGGACACGTA TTTTGTCTTT

901 GACTTGGTTA GAGTGAGGGA TCAGGAAACA CCACACTGAG GACGAGATGN NNNNNNNNNN
CTGAACCAAT CTCACCTCCCT AGTCCTTTGT GGTGTGACTC CTGCTCTACN NNNNNNNNNN

961 NTAGTGGGTG GGGGGCGGAC ATCAATAAAG AACTCTTCTG TGTGAGCCAC TGAGCACGGA
NATCACCCAC CCGCCGCGCTG TAGTTATTTT TTAGAGAAGAC ACASTCGGTG ACTCGTGCCT

1021 ATAAAGGGAT GAGASTGAGG GCAANTACCA GAAGAATAAA ATCCTTTTAA GAGATGAAGA
TATTTCCCTA CTCTCACTCC CGTTNATGGT CTTCTTATTT TAGGAAAATT CTCTACTTCT

1081 TTGTTATGAG CACAGTGTGT GGNTTCAAAA ATCTTTTAAC AACCCCAAGG TGAAGCTAGT
AACAATACTC GTGTACACACA CCNAAGTTTT TAGAAAATTG TTGGGGTTCC ACTTCGATCA

1141 TGGAAGATAT TTGAATTTGT TTAAACCCAT CTGGTCCTAG CCCTATTCTT TGAATCCGAA
ACCTTCTATA AACTTAAACA AATTTGGGTA GACCAGGATC GGGATAAGAA ACTTAGGCTT

1201 GAGGTCAAGA ATTCCGAGCA GASTGSACTA CCTGTGATAC CTTAGACTAG TCCTGTGTAT
CTCCAGTTCT TAAGGCTCGT CTCACCTGAT GGACACTATG GAATCTGATC AGGACACATA

1261 TCAAGTCCAA TGAGAGTATC TGTAAGAGAA TAAGTGCGAA ATCCAGATCT
AGTTCAGGTT ACTCTCATAG ACATTCTCTT ATTCACGCTT TAGGTCTAGA

63/130

FIGURE 41

	10	20	30	40	50	60
1	GGATTCTGTT CCTAAGACAA	GAGCCCTAGC CTCGGGATCG	TCATTATGAT AGTAATACTA	GTCCTGTTGT CAGGACAACA	CCTACCCAAA GGATGGGTTT	TAAGACTCAT ATTCTGAGTA
61	CCCAACTACA GGGTTGATGT	TCTCAATAAT AGAGTTATTA	TAATGAAGAT ATTACTTCTA	GGAAATGAGG CCTTTACTCC	TAAAAAATAA ATTTTATTATT	ATAAATAAAT TATTTATTTA
121	AAAAGAAACA TTTTCCTTGT	TTCCCCCCCA AAGGGGGGGT	TTTATTATTT AAATAATAAA	TTTCAAATAC AAAGTTTATG	CTTCTATGAA GAAGATACTT	ATAATGTTCT TATTACAAGA
181	ATCCCTCTCT TAGGGAGAGA	AAATATTAAT TTTATAATTA	AGAAATCAAT TCTTTAGTTA	ATTATTGGAA TAATAACCTT	CTGTGAATAC GACACTTATG	CTTTAATATC GAAATTATAG
241	TCATTATCCG ASTAATAGGC	GTGTCAACTA CACAGTTGAT	CTTTCCTATG GAAAGGATAC	ATGTTGAGTT TACAACTCAA	ACTGGGTTTA TGACCCAAAT	GAAGTCGGGA CTTCAGCCCT
301	AATAATGCTG TTATTACGAC	TAAANNNNNN ATTTNNNNNN	AGTTAGTCTA TCAATCAGAT	CACACCAATA GTGTGGTTAT	TCAAATATGA AGTTTATACT	TATACTTGTA ATATGAACAT
361	AACCTCCAAG TTGGAGGTTT	CATAAAAAGA GTATTTTCTT	GATACTTTAT CTATGAAATA	AAAAGAGGTT TTTTCTCCAA	CTTTTTTTTCT GAAAAAAGA	TTTTTTTTTTT AAAAAAAAAAA
421	TCCAGATGGA AGGTCTACCT	GTTCCTCTCC CAAATGAGG	TGTCAGGCAG ACAGTCCGTC	GCNGAGTGCA CGNCTCACGT	GTGGTGCCAT CACCACGGTA	CTCGGCTCAC GAGCCGAGTG
481	TGCAACCTCC ACGTTGGAGG	ACCTCCCATG TGGAGGGTAC	TTTAAAGGAT AAGTTCCCTA	TCTCCTTCCT AGAGGAAGGA	CAGTCTCCTG GTCAGAGGAC	AGTAGCTGGG TCATCGACCC
541	ATTACAGGTG TAATGTCCAC	TGCACCACCA ACGTGGTGGT	CACCCAGCTA GTGGGTGAT	ATTTTGTAT TAAAAACATA	TTTTAATAGA AAAATTATCT	GACAGGGTTT CTGTCCCAA
601	CGATCGATGT GCTAGCTACA	TGGCCAGGCT ACCGGTCCGA	AGTCTCGAAC TCAGAGCTTG	TCCTGACCTC AGGACTGGAG	TAGGTGATCC ATCCACTAGG	ACCCGCTCAG TGGGCGAGTC
661	CTCCCAAAGT GAGGGTTTCA	TGTAGAATTA ACATCTTAAT	CACGTGTGAG GTGCACACTC	GCACTGCGCC CGTGACGCGG	TTGCCAGGAG AACGGTCCTC	ATACATTTT TATGTAAAAA
721	GATAGGTTTA CTATCCAAAT	ATTTATAAAG TAAATATTTT	ACACTGCACA TGTGACGTGT	GATTTGAGTT CTAAACTCAA	GCTGGGAAAT CGACCCTTTA	GCACGGATTC CGTGCCTAAG
781	CAGTATGCA GTCATACGT					

64/130

FIGURE 42

10 20 30 40 50 60
1 AATCAAAATA AAACAGTTAA AGTTTCAATTA CTATTAATCAA ACACAAAATA AATGAATATTT
TTAGTTTAT TTTGTCAATTT TCAAACTAAT GATAATAGTT TGTGTTTT TTACTATATAA
61 ATCTTTTATG TCAGTAGAGG CTTAAATGAAT CCTTCAAGGAT TTTGATGATA GTATCAGATA
TAGAAATAC AGTCATCTCC CAATTAATTA GGAAATCTTA AAACACTACTAT CATAGTCTAT
121 CCCAGCACTA TGCATAGAAGT TCTGAAGAAT TCACGAGATG AATAAATCAC AGATTCTGTC
GGTCTGTGAT ACCATCTTCA ACACCTCTTA AGTGCCTAC TTATTTAGTG TCTAAGACAG
181 CTCAAAATGG TTAGATCTAT TCAGGAACA AAGCTAATAA AACCCACCA ATAACTAAAA
GAGTTTACC AATCTAGATA AGTCCTTTCT TTCCGATTTT TTGGGGTGGT TATTGATTTT
241 ATCAACCAA TGAAAAACA CAATCATAA ATAAGTAAGT ACCATAGAA AGAAAAGCTC
TAGTTGGTTT ACTTTTGT GTTAGTATTT TATTCATTTCA TGGATATCTT TCTTTTCGAG
301 AGAGGAGGTA AAAAGAATCT CCTTAAAGG AATACATAT ACTGTAAAC TGTGACTGAT
TCTCCTCCAT TTTTCTTAGA GGAATTTTCC TTATGATATA TGACATTTTG AACTGACTA
361 AGAAGGA
TCTTCCTT

65/130

FIGURE 43A

	10	20	30	40	50	60
1	TATGGGAAAG ATACCCTTTC	TTTTTCAGAGG AAAAGTCTCC	AAATAAGGTA TTTATTCAT	AGGGAAAAGT TCCCTTTTCA	TATCTCTTTT ATAGAGAAAA	TTTCTCTCCC AAAGAGAGGG
61	CCAATGTAAA GGTTACATTT	AAGTTATAGT TTCAATATCA	GGGTTTTTACA CCCCAAATGT	TGTGTAGAAT ACACATCTTA	CATTTTCTTA GTAAAAGAAT	AAACTTTATG TTTGAAATAC
121	AATACCATTA TTATGGTAAT	TTTTCTTGTA AAAAGAACAT	TTCTGTGACA AAGACACTGT	TGCCACCTTA ACGGTGGAAT	CAGAGAGGAC GTCTCTCCTG	ACATTTACTA TGTAATATGAT
181	GGTTATATCC CCAATATAGG	CGGGGTTAAA GCCCCAATTT	TTGAGCATT AAGCTCGTAA	GGAATTTGGC CCTTAAACCG	CAGTGTAGAT GTCACATCTA	GTTTAGAGTG CAAATCTCAC
241	AACAGAACAA TTGTCTTGTT	TTTTTCTGTG AAAAAGACAC	CTTACAGGTT GAATCTCCAA	ATGGCTGTGG TACCGACACC	CGTACAAAGAA GCATGTTCTT	GCATGCACTG CGTACGTGAC
301	GGTTTATTAT CCAAATAATA	TAACTTTCAG ATTGAAAGTC	TATCTTTGTT ATAGAAACAA	TTAAATATT AATTTATAAA	TCTACAAAAA AGATGTTTTT	TGTTTACTAA ACAAATGATT
361	ATTAAATTGT TAATTTAACA	AGTATGAATT TCATACTTAA	GTTATAAATA CAATATTTAT	ATGAGGAAAA TACTCCCTTT	CATTTACACA GTAAATGTGT	TAGCAAATTT ATCGTTTAAA
421	AAAAATTACT TTTTTAATGA	GTCAATTTGAT CAGTAAACTA	TTGTTAATAT AATTAATTATA	ATTTTCTCT TAAAAAGAGA	TTAGTGGGAA AATCACCCTT	ATTAAATTAA TAATTTAATT
481	AAAATTCCTT TTTTAAGGAA	TGCACTGTCA AGCTGACAST	GACAATAGGA CTGTTATCC	TTGCTGTGGT AACGACACCA	CTACTTGCTT GATGAACGAA	ATTATATTTG TAATATAAAC
541	TAGAGTCTAG ATCTCAGATC	AATGCAATCT TTACGTTASA	CACTACACTA GTGATCTGAT	TAGACATCTC ATCTGTAGAG	ANNCTAACGT TNNGATTGCA	AGGACAATTC TCCTGTTAAG
601	TGAGAAACTA ACTCTTTGAT	TTCCAGACCT AAGGTCTGGA	CCTTATGGGC GGAATACCCG	TTAGCCAAGG AATCGGTTCC	NTATCCTTCA NATAGGAAGT	GCTGGCATTG CGACCGTAAC
661	CAGGGTGACT GTCCCACTGA	TCTNCCTCNV AGANGGAGNN	AATCCAGCTC TTAGGTCGAG	TCTNTCACAG AGANAGTGTC	ATGTGATCCA TACACTAGGT	AGAGACACTC TCTCTGTGAG
721	ACAATTAATC TGTTAATTAG	AACTAGCATT TTGATCGTAA	CTAAATTTCA GATTTAAAGT	ATTCCAGATC TAAGGTCTAG	TATTACCTTA ATAATGGAAT	ATATGGTAGC TATACCATCG

66/130

FIGURE 43B

781 TGAAGCTTTN NTCAGTGTCA ATTCTGATCA GATATATGAC AATTTTAAAT TATTTGCAGT
ACTTCGAAAN NAGTGACAGT TAAGACTAGT CTATATACTG TTAAAATTTA ATAAACGICA

841 GTGTAAGAAA CGCTTCAGGT AGTTTAAATT TAAGGCT
CACATTCTTT GCSAAGTCCA TCAAATTTAA ATTCCGA

67/130

FIGURE 44A

	10	20	30	40	50	60
1	CTCCTTTGGC GAGGAAACCG	CCCTGCCAGC GGGACGGTCG	TGGGCATTTT ACCCGTAAAA	TAACCTAGTT ATTGGATCAA	TACACAGTGT ATGTGTCACA	CTTTTTTTTCC GAAAAAAAGG
61	TTATTTTAAA AATAAAATTT	TTGTTTGTTC AACCAACAAG	CAGATTCCGGT GTCTAAGCCA	AATATCAATT TTATAGTTAA	TTTAATATTA AAATTATAAT	CACTTAAATG GTGAATTTAC
121	AGTACCAGAA TCAATGCTCT	CTTTATCTTC GAAATAGAAG	AACCTTTTTC TTGGAAAAAG	TCATTAGGCC AGTAATCCGG	TACAACATAG ATGTTGTATC	GACATCTCGG CTGTAGAGCC
181	ATAGAATTTT TATCTTAAAG	CTTTTCTTTT GAAAAGAAAA	TGCTACTATA ACGATGATAT	AGCTGCTAAA TCGACGATTT	ATCCTCAGAA TAGGAGTCTT	CATCAGATTT GTAGTCTAAA
241	AGAAATGTTT TCTTTACAAG	TTATTAGTGG AATAATCACC	TAGTGAGCAT ATCACTCGTA	TTGCTATTTT AACCATAAAG	CTACCACTAG GATGGTGATC	CTTACAAATA GAATGTTTAT
301	TAATAAGCAA ATTATTCGTT	GTAGACCCCA CATCTGSSST	CAGGCCAAAT GTCCSGTTTA	TCCTATTTGT AGGATAAACA	TCTACAGTCG AGATGTCAGC	AAAGGGAATT TTTCCCTTAA
361	TTTTAAAAAT AAAATTTTAA	TAATTTCCAC ATTAAAGGTG	TAAAGAGAAA ATTTCTCTTT	AATATATTAA TTATATAATT	CAATCAAATT GTTAGTTTAA	GACAGTCGAT CTGTCAGCTA
421	TTTAATTTCT AAATTAACCA	ATGTTTAAAT TACACATTAA	TTTTTCCCTC CAAAAGGGAG	ATTATTTATA TAATAAATAT	ACAATTCATA TGTTAAGTAT	CTACAATTTA GATGTTAAAT
481	ATTTAGTAAA TAAATCATT	CATTTTGTGA GTAAAAACAT	GACCATATTT CTGGTATAAA	AAAACAAAGA TTTTGTTTTCT	TACTGAAAGT ATGACTTTCA	TAATATAAAC ATTATATTTG
541	TTAGTGCATG CTTCACGTAC	CTCTCTGTAG GAGAGACATC	GCCACAGCCA CGGTGTCCGT	TAACCTGTAA ATTGGACATT	GCACAGAAAA CGTGTCTTTT	ATTTGTTCTG TAAACAAGAC
601	TTACTCTAAA AATGAGATTT	CATCTACACT GTAGATCTGA	GGCCAAATTC CCGGTTTAAAG	CAATGCTCGA GTTACGAGCT	ATTTAACCCC TAAATTGGGG	GGGATATAAC CCCTATATTG
661	CTAGTAAATG GATCATTTAC	TGTCCTCTCT ACAGGAGAGA	GTCAAGGTGG CAGTTCCACC	GCATGTCACA CGTACAGTGT	GAATACAGAA CTTATGTCTT	CAATCAATGG GTTAGTTACC
721	TATTCATAAA ATAAGTATTT	GTTTTAAGAA CAAAATTCTT	AATGATTCTA TTACTAAGAT	CACATGTAAA GTGTACATTT	ACCCACTATA TGGGTGATAT	ACTTTTTTACA TGAAAAATGT

68/130

FIGURE 44B

781 TTGGGGGAGA GAAAAAAGA GATAATTTT ACCTTACCTT ATTTCTCTCTG AAAACTTTCC
AACCCCTCT CTTTTTTTCT CTATTAAAA TGGAATGGAA TAAAGGAGAC TTTTGAAAGG

841 CATATCTGGC AATTACAATT TTCCAGAGC AATTGATTTT CATGTCCCTT TCC
GTATAGACCG TTAATGTTAA AAGGGTCTTC TTAATAAAA GTACAGGGCA AGG

69/130

FIGURE 45A

	10	20	30	40	50	60
1	GATGCTATTT CTACGATAAA	GGGCAATTTT CCCGTTAAAG	TTATTGACAG AATAACTGTC	TTTTGAAATG AAAACCTTAC	TTAGGCTTTT AATCCGAAAA	ATCTCCATTT TAGAGGTAAA
61	TTTAGTACTT AAATCATGAA	AAATTTTCCA TTTAAAAGGT	ACATGGGTGT TGTACCCACA	TGCTTGTTAT ACGAACAATA	TTTATCAGTA AAATAGTCAT	TAAAATAGAA ATTTTATCTT
121	GAGTGGTTCT CTCACCAAGA	GTTCTGGAAT CAAGACCTTA	TTAGTATATA AATCATATAT	CATGAGTATC GTACTCATAG	TAGTGTATGT ATCACATACA	CAGCCATGAA GTCGGTACTT
181	AATGAACCTT TTACTTGGA	TCAGATGTTT AGTCTACAAA	AACTTCAGGG TTGAAGTCCC	AACCTAATTG TTGGATTAAC	AGTCATTGCT TCAGTAACGA	CCAGACATTG GGTCTGTAAC
241	TTGCTTTGAA AACGAAACTT	CCCACTATAT GGGTGATATA	TNNNNNNNCT ANNNNNNNNA	CGGGCAATTA GCCCGTTACT	CTCAGTGTGG GAGTCACACC	CAAGGATACT GTTCTATGAA
301	ACTGCAGGCC TGACGTCCGG	TGTTTCTGGA ACAAAGACCT	AGGCACTGGA TCCGTGACCT	CTCCTCTGAT GAGGAGACTA	GCAAACCTTG CGTTTGAAAC	GCCAGGGACT CGGTCCCTGA
361	CCTTGATAGC GGAACATATC	TCTTAAATAG AGAACTTATC	ATGCTGCACC TACGACGTGG	AACACTCTCT TTGTGAGAGA	TTCTTTTCTC AAGAAAAGAG	TCTTTTCTCT AGAAAAAGAA
421	TATTCAATAT ATAAGTTATA	TAGACTACAA ATCTGATGTT	GCACTCTAAT CGTCAGATTC	GACTTCTCAG CTGAAGASTC	GGTTTCTAGC CCAAAGATCG	TCTCTCTCAT AGAGAGAGTA
481	TTACACACATG AAGTGTGTAC	CTTTCTTAGT GAAAGSATCA	AATCTCTACT TTAGAGATGA	CATATATCTT GTATATAGAA	ACTGCTACGC TGACGATGCG	TGGGGCCAGA ACCCCGGTCT
541	TAAACNNNNN ATTGNNNNNN	CTTCCATTTT GAAGGTAAAA	GTCTTTTATCT CAAAAATAGA	CTATTCTTCT GATAAGAAGA	TCCCCTTCTG AGGGGAAGAC	CTTTCATTAT GAAAGTAATA
601	TGAAACTTTT ACTTTGAAAG	TGCTTTCATT ACGAAAGTAA	ATTGAAACTT TAACTTTGAA	TCCCAGATTT AGGGTCTAAA	GTTCTGCTTA CAAGACGAAT	ACCTGGCATT TGGACCGTAA
661	GGAACGTGTT CCTTGACAAA	CCTCTTCCCT GGAGAAGGGA	GTGCTGCTTT CACGACGAAA	CTCCCATTCG GAGGGTAACG	CATGTCCTTT GTACAGGAAA	TTTTTTTTTT AAAAAAAAAA
721	TTTTTTTTTT AAAAAAAAAA	TGAGACAGTG ACTCTGTCAC	TCACTCTGTT AGTGAGACAA	GCCCAGGCTG CGGGTCCGAC	GAGTGCAATG CTCACGTTAC	GTGCAATCTT CACGTTAGAA

70/130

FIGURE 45B

781 GGCCACTGCA ACCCCGACTC CGGGTTCAAG TGATTCTCTA CCTGCCTCAG CCTCCTGAGT
CCGGTGACGT TGGGGCTGAG GCCCAAGTTC ACTAAGAGAT GGACGGAGTC GGAGGACTCA

841 AGCTGGGATT ACAGGTGCCA CCACTATGCC GGCTGATTTT GTATTTTAGT AGAGATGGGT
TCGACCCCTAA TGTCCACGGT GGTGATACGG CCGACTAAAA CATAAAATCA TCTCTACCCA

901 TCACATGCAG ATCAGCTGTT CCGACTCTGA CCAGNNNNNN NNNNNNNNNN ATCAAAGTCA
ASTGTACCTC TAGTCGACAA GGCTGAGACT GGTNNNNNNN NNNNNNNNNN TAGTTTCAGT

961 GCCAAAGTGC TAGGCTTAGA GTAATTGTGT AATTTCCACA CAAGTGCAAC CTAGTGTAAT
CGGTTTCACG ATCCGAATCT CATTAAACACA TTAAAGGTGT GTTCACGTTG GATCACATTA

1021 GCGTCAAGAA TGTNNNTATG AATGTCTCGA ACGTTAGTAA CTAATAACAA GTAGTTAGTT
CGGAGTTCTT ACANNNTATC TTACAGAGCT TCGAATCATT GATTATTGTT CATCAATCAA

1081 TATAGATGTA TCCTAGTATG TAGCA
ATACTACAT AGGATCATAC ATCGT

71/130

FIGURE 46A

	10	20	30	40	50	60
1	CACAAAAAAA GTGTTTTTTT	GATTATTAGC CTAATAATCG	CACAAAAAAA GTGTTTTTTT	CCTTGAAGTA GGAAC TTCAT	ACGCATTAAA TGC GTAATTT	ATGTTAATGG TACAATTACC
61	ATTCAC TTTA TAAGTGAAAT	TTGAGCATCT AACTCGTAGA	GCTCATAATA CGAGTATTAT	CTTTAATGAG GAAATTACTC	TGCAAAGTGC ACGTTTCACG	TTTGAATATA AACTTATAT
121	ATACGTCATT TATGCAGTAA	TAAACCTTAC ATTTGGAATG	CATAATTCTG GTATTAAGAC	AGGAATTGCT TCCTTAACGA	ACCTCCACTT TGGAGGTGAA	CACAGATGGG GTGTCTACCC
181	GCACAGGAGG CGTGTCTCTC	CTTAGATAAC GAATCTATTG	ATGCCCAAAG TACGGGTTTC	TCATGCTTCT AGTACGAAGA	AGTAAATGGA TCATTTACCT	TATAATTAAG ATATTAATTC
241	ATTCAAATTA TAAGTTTAAT	TTGATAAGAA AACTATTCTT	TTTGATCTGC AACTAGACG	CTTACCAATA GAATGGTCAT	TCTAGTAGTA AGATCATCAT	AATCTAAAAG TTAGATT TTC
301	CGCTTTCCAG GCGAAAGGTC	AGCATGTGCT TCGTACACGA	GTTGATAGAG CAACTATCTC	CTTGATGTCT GAACTACAGA	AACTCTCTGA TTGAGAGACT	AATTTTCCAT TTAAAAGGTA
361	TCTTATTTGT AGAATAAACA	CTCACTGGTA GAGTGACCAT	TATAGTTATT ATATCAATAA	TTTTACTACT AAAATGATGA	TTCATACACC AAGTATGTGG	TACTAAGAAG ATGATTCTTC
421	ACAGGAGGAT TGTCTCTCTA	CAAAGATAGG GTTTCTATCC	ATTTCAATTA TAAAGTAAAT	GAATGGCTAA CTTACGGATT	AGCTTCACGT TCGAAGTGCA	ATTTTAATTC TAAAATTAAG
481	AGAATAAGAT TCTTATTCTA	TCAGGCAGAC AGTCCGTCTG	CACCAGTATA GTGGTCATAT	TGGCATGGTC ACGGTACCAG	CCTGGTTATC GGACCAATAG	TTTCAGCAGG AAAGTCGTCC
541	TGACCGAGAA ACTGGCTCTT	AGAAAACATG TCTTTTGTAC	GTAATGTTTA CATTACAAAT	TGAAATGGTG ACTTTACCAAC	GGTTCTTGTA CCAAGAACAT	GTTTCACTTC CAAAGTGAAG
601	AACATATCTG TTGTATAGAC	CCTTTACTGT GGAAATGACA	ATTAAGATGA TAATTCTACT	TGGATTAACT ACCTAATTGA	TATTCTTGAT ATAAGAACTA	ATGGGCATGT TACCCGTACA
661	AAAACAATAT TTTGTGTTATA	ACTTTTACTA TGAAAATGAT	AACAGCTACA TTGTCGATGT	GAGAGACAAA CTCTCTGTTT	TGTGTTTCCA ACACAAAGGT	GACAAACTTA CTGTTTGAAT
721	AGAGACTGAG TCTCTGACTC	TGTTCAAAC T ACAAGTTTGA	GAATAATCTC CTTATTAGAG	GACCTTAATT CTGGAATTAA	GTAAC TATAT CATTGATATA	TTTATGAAAT AAATACTTTA

72/130

FIGURE 46B

781 CCAGCTGTAA GGCAAAACAG ACTCTTGGCT ACACGGCATT TGTCTGTTAA TGATACTCAA
GGTCGACATT CCGTTTTGTC TGAGAACCGA TGTGCCGTAA ACAGACAATT ACTATGAGTT

841 COTTAACCGT CACTTAATAA TGCTGAATAA TGTCATTAAT CTGAGATGTT AGTATGATCA
GGAATTGGCA GTGAATTATT ACGACTTATT ACAGTAATTA GACTCTACAA TCATACTAGT

901 ATGGGAATCA CTGCTGAGCT CTCGAAGCCC
TACCCTTAGT GACGACTCGA GAGCTTCGGG

74/130

FIGURE 47B

CCA ACT GAA GAC TTC TTT AAA TTG GAA CAG CAC ATG AAA ATC AAT TTC TCT GAG AAA ATT GTA ATT GGC AGA TAT GGG AAA GTT TTC AGA 630
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asp Gys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg 210
 GGA AAT AAG GTT AAA AAT GCG CAG CTG GCA GCG GCG AAA GCA GGC ATT CTG TAC TCC GAC CCT GCT GAC TAC TTT GCT CCT GCG GTG AAG 720
 Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gln Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys 240
 TCC TAT CCA GAT GAT TGG AAT GTT CCT GCA GGT GGT GTC CAG CGT GGA AAT ATC CTA AAT CTG AAT GGT GCA GGA CAC CCT CTC ACA CCA 610
 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Val Gln Arg Gln Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro 270
 GGT TAC CCA GCA AAT GAA TAT CCT TAT ACG CGT GCA ATT GCA GAG CCT GTT GGT CTT CCA AGT ATT CCT GAT CCA ATT GCA TAC TAT 900
 Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Gln Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr 300
 GAT GCA CAG AAG CTC CTA GAA AAA ATG GGT GCG TCA CCA CCA GAT AAT AAT TGT AAT GCA AGT CTC AAA GTG CCG TAC AAT GTT GCA 990
 Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly 330
 CCT GGC TTT ACT GGA AAC TTT TCT ACA CAA AAA GTC AAG ATG CAC ATC CAC TCT AAT AAT GAA GTG ACA AGA ATT TAC AAT GTG ATA GGT 1080
 Pz Gly Phe Thr Gly Arg Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Gln Val Thr Arg Ile Tyr Asn Val Ile Gly 360

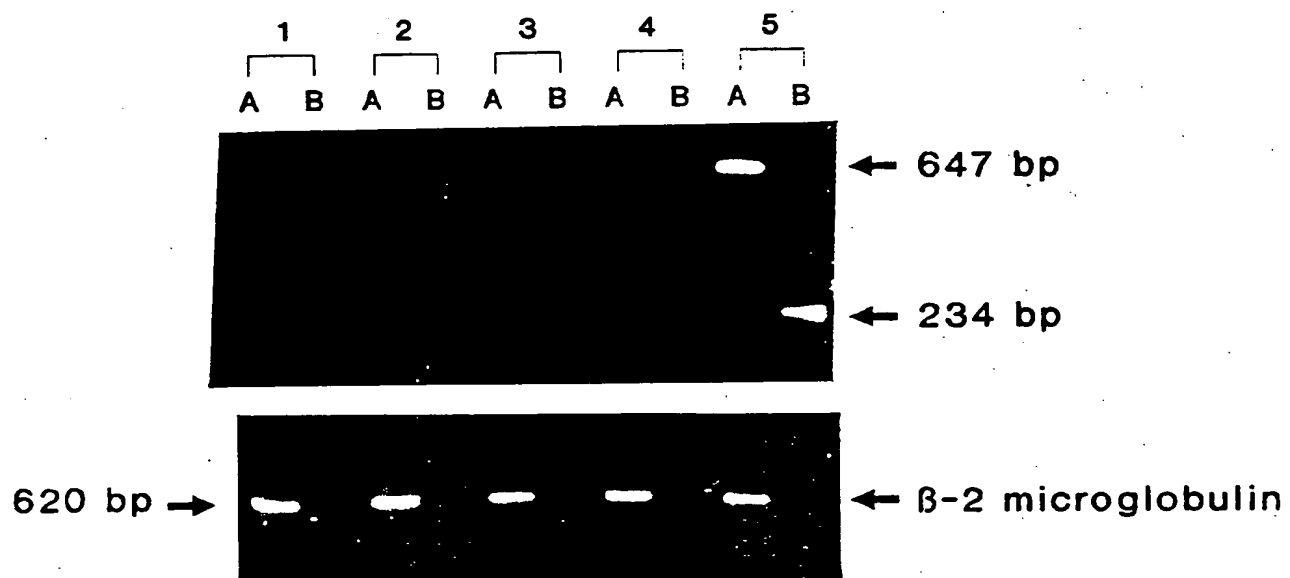
75/130

FIGURE 47C

ACT CTC AGA GCA GCA GTG GAA CCA GAC AGA TAT GTC ATT CTG GGA GGT CAC CGG GAC TCA TOG GTG TTT GGT ATT GAC OCT CAG AGT 1170	Thr Leu Arg Gly Ale Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser 390	TTT GCA AGC 1260
GGA GCA OCT GTT GTT CAT GAA ATT GTG AGG AGC TTT GGA ACA CTG AAA ANG GAA GAA GAG TGG AGA CCT AGA AGA ACA ATT TTG	Gly Ale Ale Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile Leu	Phe Ale Ser 420
TOG GAT GCA GAA TTT GGT CTT GCT TCT ACT GAG TGG GAA GAG AAT TCA AGA CTC CTT CAA GAG CGT GGC GTG OCT TAT ATT 1330	Trp Asp Ale Glu Glu Phe Gly Leu Leu Gly Ser Thr Glu Tyr Ala Glu Glu Aen Ser Arg Leu Leu Gln Glu Arg Gly Val Ale Tyr Ile 430	
AAT OCT GAC TCA TCT ATA GAA GCA AAC TAC ACT CTG AGA GTT GAT TGT ACA CGG CTG ATG TAC AGC TTG GTA CAC AAC CTA ACA AAA GAG 1440	Aen Ala Asp Ser Ser Ile Glu Gly Asp Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asp Leu Thr Lys Glu 480	
CTG AAA AGC CCT GAT GAA GGC TTT GAA GCA AAA TCT CTT TAT GAA AGT TGG ACT AAA AAA AGT OCT TCC CCA GAG TTC AGT GGC ATG CCG 1530	Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser Tyr Thr Lys Lys Ser Pro Ser Pro Ser Pro Ser Gly Met Tr 510	
AGG ATA AGC AAA TTG GCA TCT GCA AAT GAT TTT GAG GTG TTC TTC CAA CGA CTT CGA ATT OCT TCA GGC AGA CCA CGG TAT ACT AAA AAT 1620	Arg Ile Ser Lys Leu Gly Ser Gly Aen Asp Phe Glu Val Phe Phe Gln Arg Leu Glu Ile Ala Ser Gly Arg Ale Arg Tyr Thr Lys Aen 540	
TOG GAA ACA AAC AAA TTC AGC CCA TAT CCA CTG TAT CAC AGT GTC TAT GAA ACA TAT GAG TTG GTG GAA ANG TTT TAT GAT CCA ATG TTT 1710	Trp Glu Thr Aen Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu Lys Phe Tyr Asp Pro Met Phe 570	

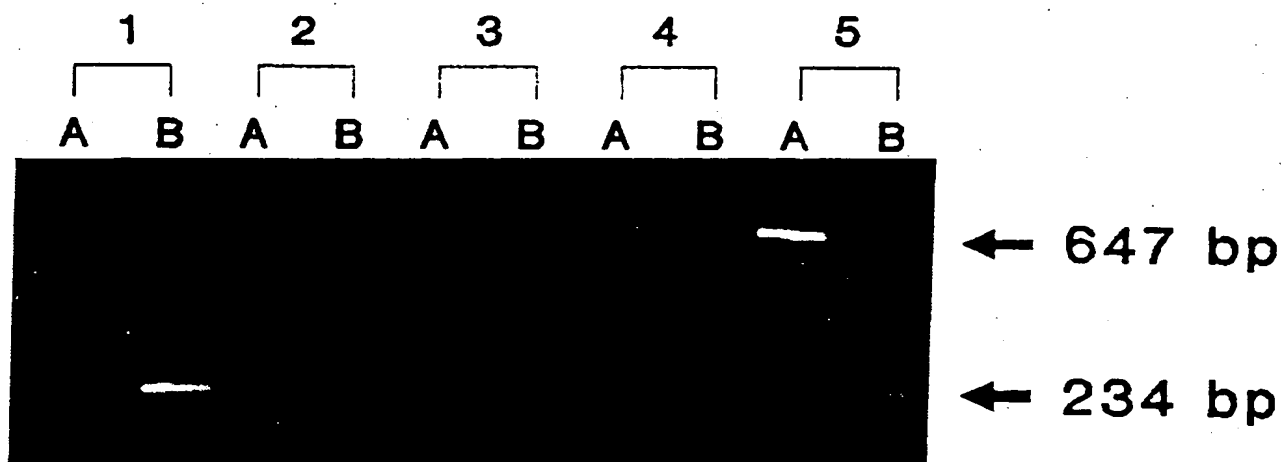
77/130

FIGURE 48



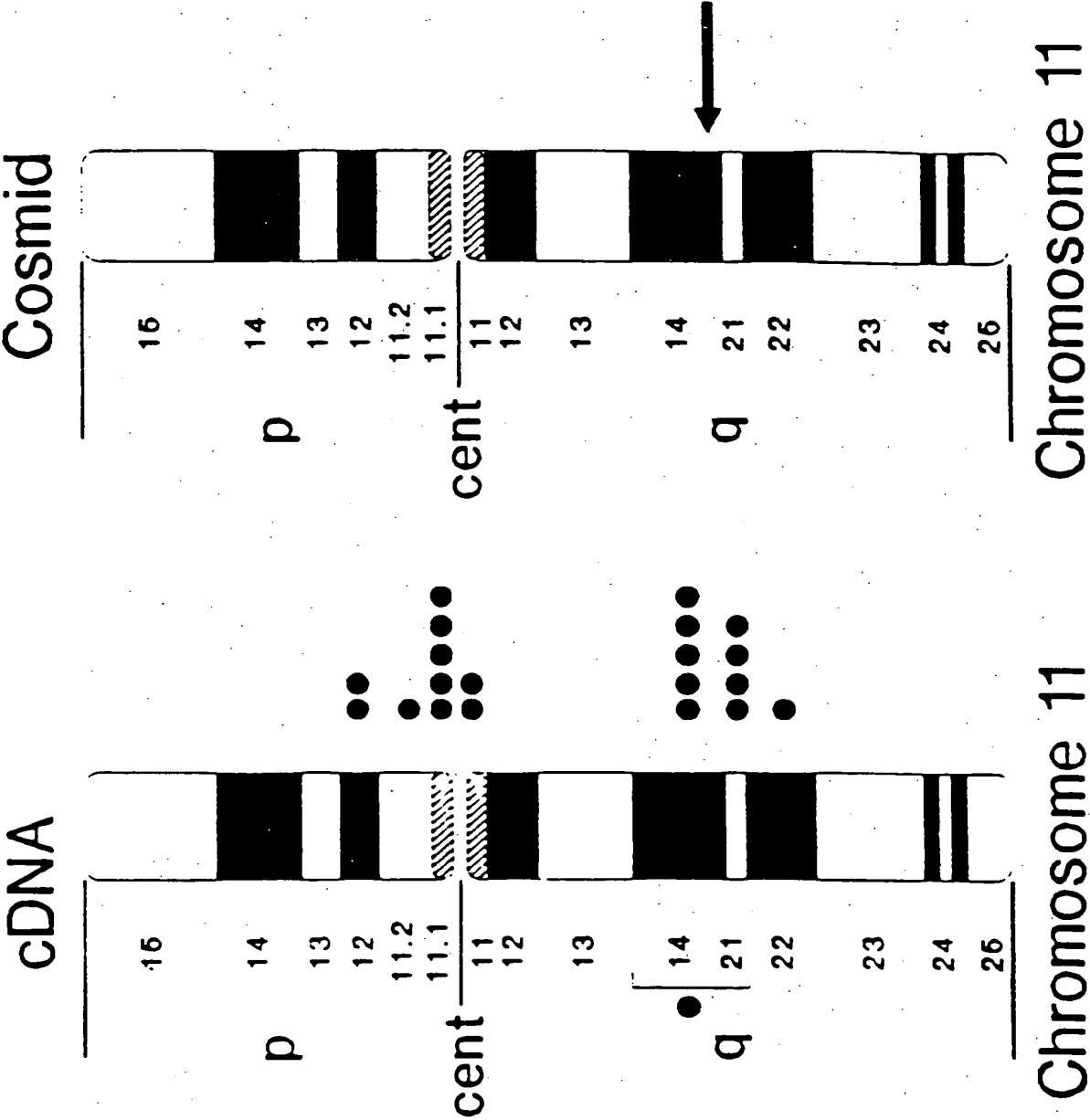
78/130

FIGURE 49



79/130

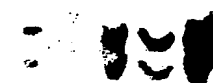
FIGURE 50



80/130

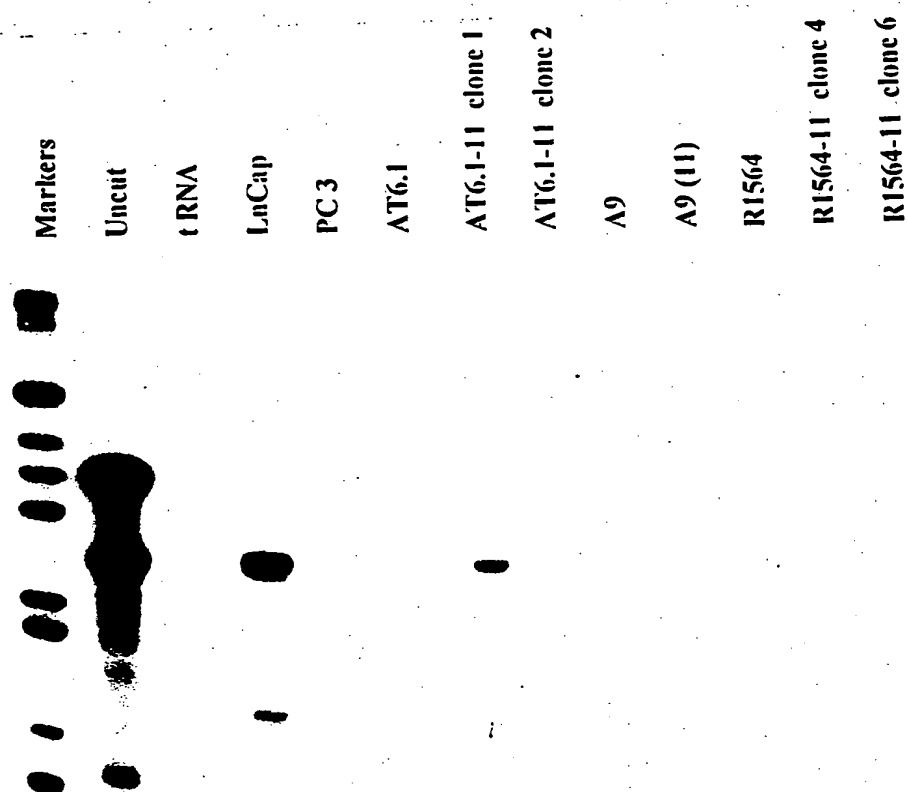
FIGURE 51

♂ ♀ M H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y



81/130

FIGURE 52



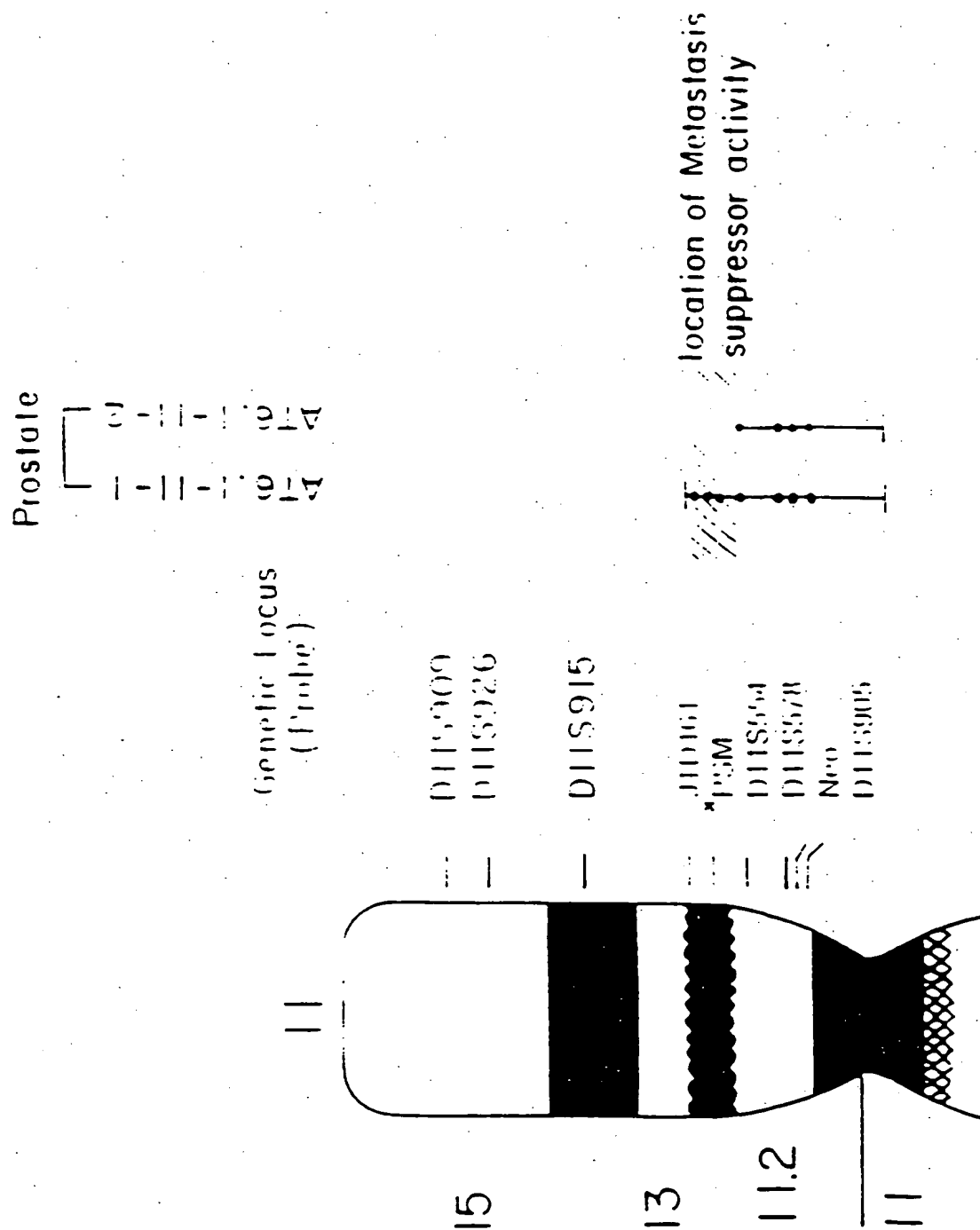
82/130

FIGURE 53

TISSUE/CELL LINE	CANCER CELL TYPE	PSM DNA	PSM RNA
HUMAN PROSTATE	N.A.	+	+
HUMAN MAMMARY	N.A.	+	-
AT6.1	RAT PROSTATIC ADENOCARCINOMA	-	-
AT6.1-11-CL1	"	+	+
AT6.1-11-CL2	"	-	-
R1564	RAT MAMMARY ADENOCARCINOMA	-	-
R1564-11-CL2	"	+	-
R1564-11-CL4	"	+	-
R1564-11-CL5	"	+	-
R1564-11-CL6	"	+	-
A9	MOUSE FIBROSARCOMA	-	-
A9(11)	"	+	-

83/130

FIGURE 54



84/130

FIGURE 55

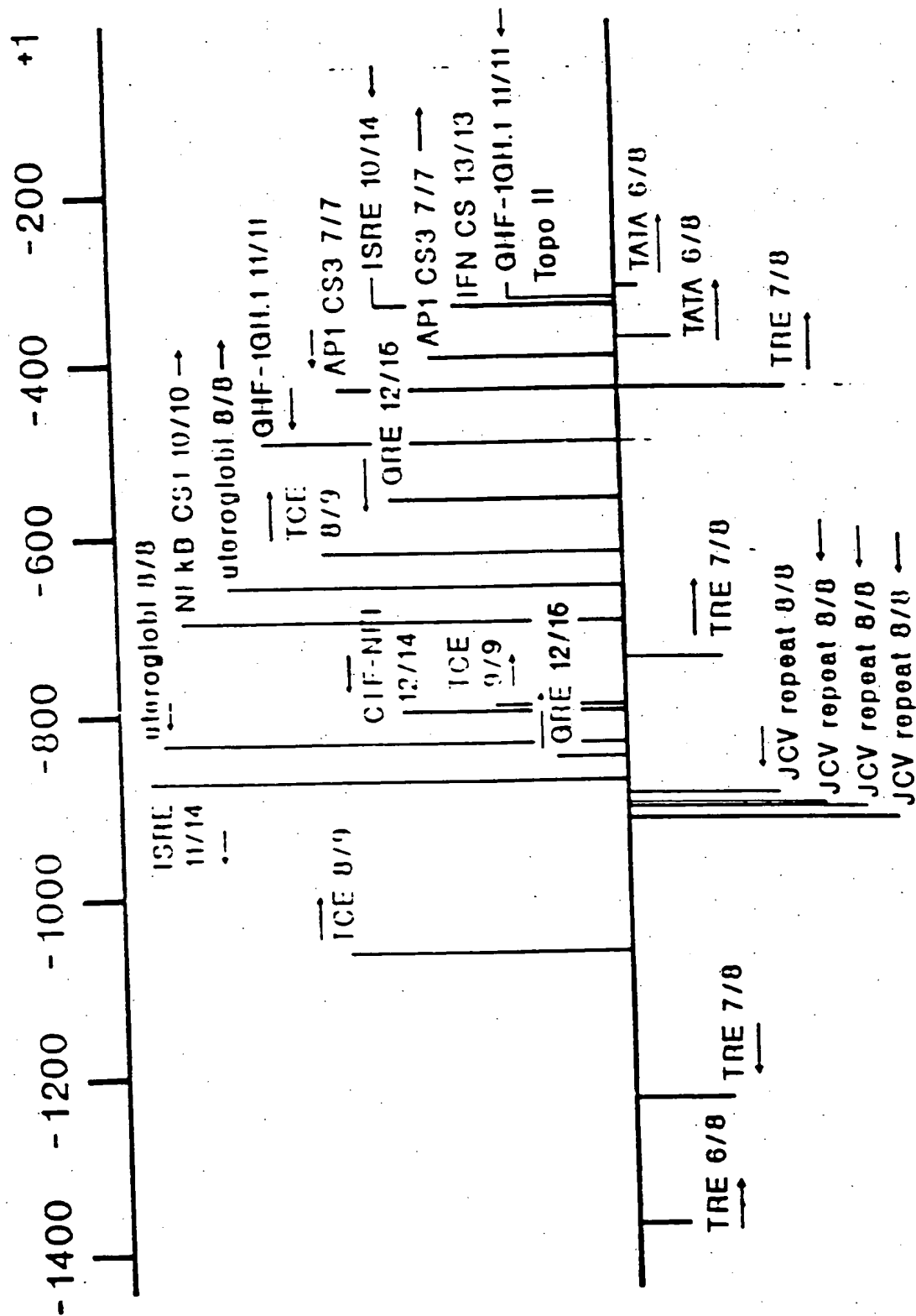
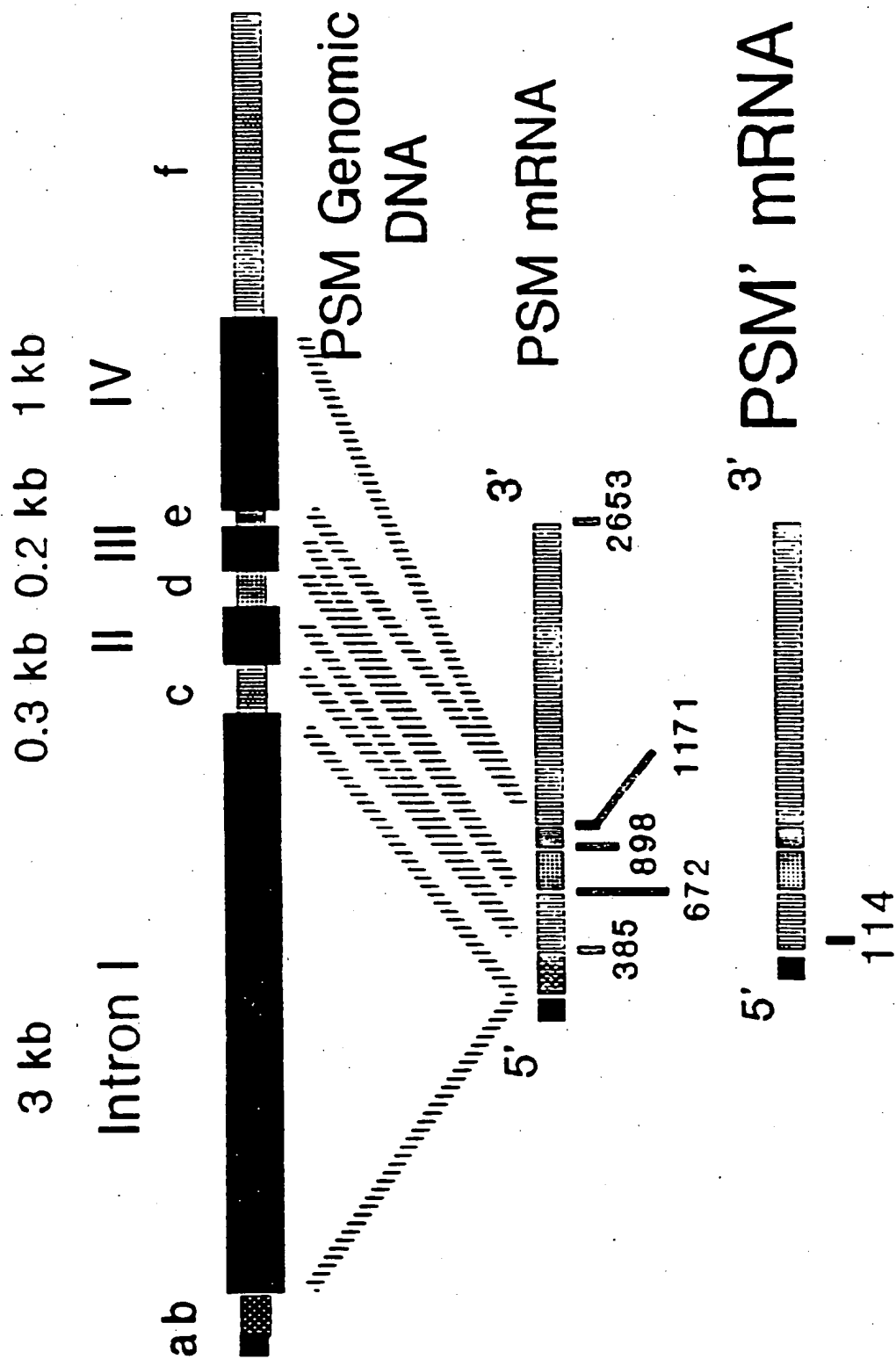


FIGURE 56

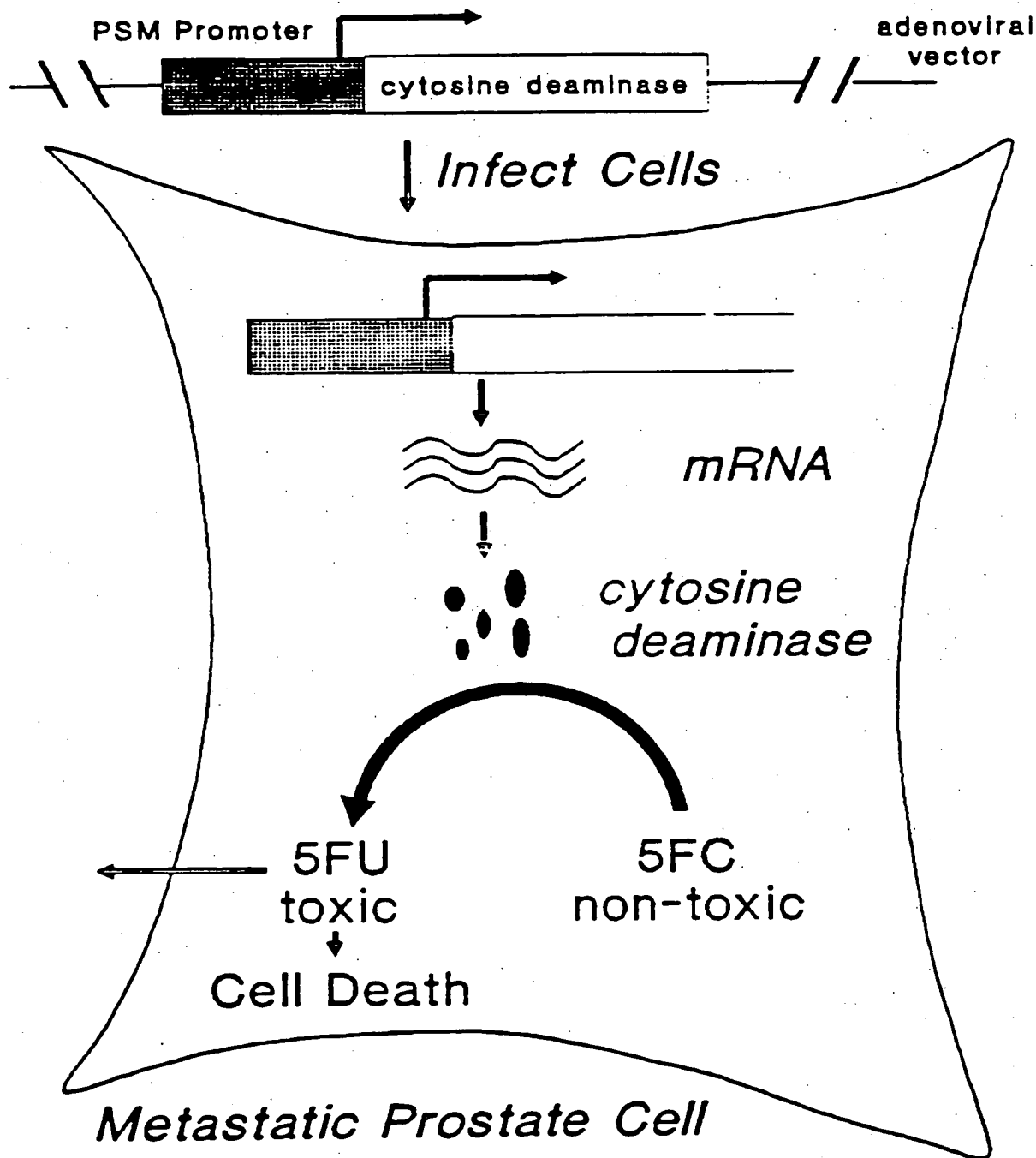
Genomic Organization of PSM Gene



86/130

FIGURE 57

Prostate Specific Promoter: Cytosine Deaminase Chimera



87/130

FIGURE 58A

	10	20	30	40	50	60
1	GCGCCTTAA	AAAAAAAAAC	TTTCTTGGAA	AATGTCCAGC	TCTTGCTTAA	ATATAAAAT
	CGCGGAATTT	TTTTTTTTTG	AAAGAACCTT	TTACAGSTCG	AGAACGAATT	TATATTTTAA
61	GAAAGGAAGA	AAGAGACTCT	CCTCTCTCCA	CTCCTATAAT	TATGAGGAAC	TTTTATTCAA
	CTTTCCTTCT	TTCTCTGAGA	GGAGAGAGST	GAGGATATTA	ATACTCCTTG	AAAATAAGTT
121	CTCTGAAATT	CTATACAATC	TCTACAATAC	TCTACTGAAT	AAAAGCAGAG	CAGAAAAAGC
	GAGACTTTAA	GATATGTTAG	AGATGTTATG	AGATGACTTA	TTTTCGTCTC	GTCTTTTTTCG
181	TGCGCTTTTT	TTCCATAGTC	GGGAATGCTT	GTCATCAGTG	TAAATCACCA	CGCGCGCCTT
	ACCGGAAAAA	AAGGTATCAG	CCCTTACGAA	CAGTAGTCAC	ATTTAGTGTT	GGCGCGGGAA
241	TTTCCTAAAG	AATATGATTG	TTATTAATAA	ACATGTAGGG	TATTATCCTC	CACTTACATT
	AAAGGATTTG	TTATAATAAC	AATAATTATT	TGTACATCCC	ATAATAGSAG	GTGAATGTAA
301	ACAAAACCAT	TTTTTAAAGC	CGGGCGTGGT	GCCTCACGCC	TSTAATSCCA	GCACTTTGGG
	TSTTTTGGTA	AAAAATTTTG	GCCCCGACCA	TGAGTGCGG	ACATTAGGGT	CGTGAACCC
361	AGGCCGAGAC	AGGGGGATCA	CGAATCTGAG	AAATCGAGAC	CATCCTGGCC	AACATGGTGA
	TCCGGSTCTG	TCCCTCTAGT	GCTTCAGCTC	TTTAGCTCTG	GTAGGACCGG	TTGTACCACT
421	AACCCCATCT	CTACTAAAAA	TACAAAAATG	ACCTGGGCGT	GGTGGCGGGC	TCCTGTAGTC
	TTGGGSTAGA	GATGATTTTT	ATTTTTTTAA	TGACCCCGCA	CCACCGCCCG	AGGACATCAG
481	CGAGCTACTC	AGGAGGCTGA	GGGAGGAGAA	TGCTTTGAAC	CGGGGAGGCG	GAGGTTGCAG
	GGTGGATGAG	TCTTCGACT	CGCTCTCTTT	ASCGAACCTG	GCCCCCTCCG	CTCCAACGTC
541	TCAGCCCAAG	TAGCGGCACT	CGACTGGAGC	CTGGTGACAG	AGTGAGACTC	CCTCAAGAAA
	AGTCGGTTCT	ATCGCGGTGA	CGTACCTCTG	GACCACTGTC	TCACTCTGAG	GGAGTTCTTT
601	GAAAGGAAGG	GAAGGGAAAG	GGAAAGGAAG	GGAGGGGAAG	GGAGGGGAGG	GGAGGGGAGG
	CTTTCCTTCC	CTTCCCTTTC	CCTTCTCTCC	CCTCCCCTTC	CCTCCCCTCC	CCTCCCCTCC
661	AAAGAAAAGA	ATACTGGAAC	TTGTTGAAGG	CAGAGACTTT	ATTTTCATAT	CCCGGCTATG
	TTTCTTTTTCT	TATGACCTTG	AACAACCTCC	GTCTCTGAAA	TAAAAGTATA	GGGCCGATAC
721	TCTGGCTACT	GTCTTACGTA	ATAGATATAA	AATCAATCTT	GGTTGGATTA	ACCAGAAGAA
	AGACCGATGA	CAGAAATGCAT	TATCTATATT	TTAGTTAGAA	CCAACCTAAT	TGGTCTTCTT

88/130

FIGURE 58B

781 TGAGAAGATA TATTCTGGTA AGTTGAATAC TTAGCACCCA GGGSTAATCA GCTTGGACAG
 ACTCTTCTAT ATAAGACCAT TCAACTTATG AATCGTGGST CCCCATTAGT CGAACCTGTG

841 GACCAGGTCC AAAGACTGTT AAGAGTCTTC TGACTCCAAA CTCAGTGCTC CCTCCAGTGC
 CTGGTCCAGG TTTCTGACAA TTCTCAGAAG ACTGAGGTTT GAGTCACGAG GGAGGTCACG

901 CACAAGCAAA CTCCATAAAG GTATCSTGTG CTGAATAGAG ACTGTAGAGT GGTACAAAAGT
 GTGTTGTTTT GAGGTATTTT CATAGGACAC CACTTATCTC TGACATCTCA CCATCTTTCA

961 AAGACAGACA TTATATTAAG TCTTAGCTTT GTGACTTCGA ATGACTTACC TAATCTAGCT
 TTCTGTCTGT AATATAATTC AGAATCGAAA CACTGAAGCT TACTGAATGG ATTAGATCGA

1021 AAATTTCAST TTTACCATGT GTAAATCAGG AAGAGTAATA GAACAAACCT TGAAGGGTCC
 TTTAAAGTCA AAATGGTACA CATTTAGTCC TTCTCATTAT CTTGTTTGOA ACTTCCCAGG

1081 CAATGGTGAT TAAATGAGGT GATGTACATA ACATGCATCA CTCATAATAA GTGCTCTTTA
 GTTACCACTA ATTTACTCCA CTACATGTAT TGTACGTAGT GAGTATTATT CAGGAGAAAT

1141 AATATTAGTC ACTATTATTA GCCATCTCTG ATTAGATTTG ACAATAGGAA CATTAGGAAA
 TTATAATCAG TGATAATAAT CGGTAGAGAC TAATCTAAAC TGTATCTCTT GTAATCCTTT

1201 GATATAGTAC ATTCAAGATT TTGTTAGAAA GAGATGAAGA AATTCCTTTC CTTCTGCCCC
 CTATATCATG TAAGTCCTAA AACAATCTTT CTCTACTTCT TTAAGGGAAG GAAGGACGGG

1261 TAGGTCACTT AGGAGTTGTC ATGGTTTCAAT GTTGACAAAT TAATTTTCCC AAATTTTTC
 ATCCAGTAGA TCCTCAACAG TACCAAGTAA CAACTGTTTA ATTAAGGAGG TTTAAAGAGT

1321 CTTTGCTCAG AAAGTCTACA TCGAAGCACC CAAGACTGTA CAATCTAGTC CATCTTTTTC
 GAAACGAGTC TTTCAAGATG AGCTTCGTGG GTTCTGACAT GTTAGATCAG GTAGAAAAAG

1381 CACTTAATTC AATCTGTGCT CTCCCTTTCT CAAAGCAAAC TGTCTGCTAT TCCTTGAATA
 GTGAATTGAG TATGACACGA GAGGGAAAGA GTTTCGTTTG ACAAGCGATA AGGAACCTAT

1441 CACTCTGAGT TTTCTGCCTT TGGCTACTCA GCTGGCCCAT GGGCCCTAAT GTTCTCTCTC
 GTGAGACTCA AAAGACGGAA ACGGATGAST CGACCGGTA CCGGGGATTA CAAAGAAGAG

1501 ATCTCCACTG GGTCAAATCC TACCTGTACC TTATGTTTCT GTTAAAGGCA GTGCTTCCAT
 TAGAGGTGAC CCAGTTTAGG ATGGACATGG AATACCAAGA CAATTTTTCGT CACGAAGGTA

1561 AAAGTACTCC TAGCAAATGC ACGGCTCTC TCACGGATTA TAAGAACACA GTTTATTTTA
 TTTCAATGAG ATCGTTTACG TGCCGGAGAG AGTGCCCTAAT ATTCTTGTGT CAAATAAAAT

1621 TAAAGCATGT AGCTATTCTC TCCCTCGAAA TACGATTATT ATTATTAAGA ATTTATAGCA
 ATTTCTGTACA TCGATAAGAG AGGGAGCTTT ATGCTAATAA TAATAATTCT TAAATATCGT

1681 GGGATATAAT TTGTATGAT GATTCTTCTG GTTAATCCAA CCAAGATTGA TTTTATATCT
 CCTATATTA AACATACTA CTAAGAAGAC CAATTAGGTT GGTCTAATCT AAAATATAGA

1741 ATTACGTAAG ACAGTAGCCA GACATAGCCG GGATATGAAA ATAAAGTCTC TGCCCTCAAC
 TAATGCATTC TGTATCGGT CTGTATCGGC CCTATACCTT TATTTACAGAG ACGGAAGTTC

1801 AAGTTCCAGT ATTCTTTTCT TTCTCTCCCT CCGCTCCCTT CCGTCCCTT CCGCTTCCCT
 TTCAAAGTCA TAAGAAAGAA AAGGAGGGGA GGGGAGGGGA GGGGAGGGGA GGGGAAAGGA

1861 CCGTTCCCT TCCCTTCCCT TCTTTCTTGA GGGAGTCTCA CTCTGTCAAC AGGCTCCAGT
 GGGAAAGGGA AAGGAAGGAA AGAAAGAACT CCTCAGACT GAGACAGTGG TCCGAGGTCA

89/130

FIGURE 58C

1921 GCAGTGGCGC TATCTTGGCT GACTGCAACC TCGCCCTCCC CGGTTCAAGC GATTCTCCTG
 CGTCACCGCG ATAGAACCGA CTGACGTTGG AGCGGGAAGG GCCAAGTTCC CTAAGAGGAC

1981 CCTCAGCCTC CTGAGTAGCT GGGACTACAG GAGCCCGCCA CCACGCCCCAG CTAATTTTTC
 GGAGTCGGAG GACTCATCGA CCCTGATGTC CTCGGGCGGT GGTCGGGTC GATTAAAAAC

2041 TATTTTTAGT AGAGATGGGG TTTCACCATG TTGGCCAGGA TGGTCTCGAT TTCTCGACTT
 ATAAAAATCA TCTCTACCCC AAAGTGGTAC AACCGGTCCT ACCAGAGCTA AAGAGCTGAA

2101 CGTGATCCGC CTGTCTGGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACCACGCC
 GCACTAGGCG GACAGACCGG GAGGGTTTCA CGACCCTAAT GTCCGCACTC GGTGGTGGCG

2161 CGGCTTTAAA AAATGGTTTT GTAATGTAAG TGGAGGATAA TACCCTACAT GTTTATTAAAT
 GCGAAAAATT TTTACCAAAA CATTACATTC ACCTCCTATT ATGGGATGTA CAAATAATTA

2221 AACATAATA TTCTTTAGGA AAAAGGGCGC GGTGGTGATT TACACTGATG ACAAGCATTG
 TTGTTATTAT AAGAAATCCT TTTCCCGCG CCACCACTAA ATGTGACTAC TGTTCGTAAG

2281 CCGACTATGG AAAAAAGCG CAGCTTTTTTC TGCTCTGCTT TTATTCAGTA GAGTATGTA
 GGCTGATACC TTTTCTTCGC GTCGAAAAAG ACGAGACGAA AATAAGTCAT CTCATAACAT

2341 GAGATTGTAT AGAATTCAG AGTGAATAA AAGTTCCTCA TAATTATAGG AGTGGAGAGA
 CTCTAACATA TCTTAAAGTC TCAACTTATT TTCAAGGAGT ATTAATATCC TCACCTCTCT

2401 CGAGAGTCTC TTTCTTCCTT TCATTTTTAT ATTAAAGCAA GAGCTGGACA TTTTCCAAGA
 CCTCTCAGAG AAAGAAGGAA AGTAAAAATA TAAATTCOTT CTCGACCTGT AAAAGGTTCT

2461 AAGTTTTTTT TTTTAAAGGC GCCTCTCAAA AGGGGCGCGA TTTCTTCTC CTGGAGGCAG
 TTCAAAAAAA AAAAATTCGG CGGAGAGTTT TCCCGGCGCT AAAGGAAGAG GACCTCCGTC

2521 ATGTTGCTC TCTCTCTCGC TCGGATTGGT TCAGTGCACT CTAGAAACAC TGCTGTGGTG
 TACAACGGAG AGAGAGAGCG AGCCTAACCA ASTCAGCTGA GATCTTTGTG ACGACACCAC

2581 GAGAAACTGG ACCCCAGGTC TGGAGCGAAT TCCAGCCTGC AGGGCTGATA AGCGAGGCAT
 CTCTTTGACC TGGGGTCCAG ACCTCGCTTA AGGTCCGAGC TCCCGACTAT TCGCTCGTAA

2641 TAGTGAGATT GAGAGAGACT TTACCCCGCC GTGGTGCTTG GAGGGCGCGC AGTAGAGCAG
 ATCACTCTAA CTCTCTCTGA AATGGGGCGG CACCACCAAC CTCCCGCGCG TCATCTCTCT

2701 CACACACAGG CGGGGTCCCG GAGGSCCGGC TCTGCTCGCG CGGAGATGTG GAATCTCCTT
 GTGCTGTCCG CGCCCAAGGC CCTCCGSCCG AGACGAGCGC GGCTCTACAC CTTAGAGGAA

2761 CACGAAACCG ACTCGGCTGT GGCACCCCGC CGCCGCCCCG GCTGGCTGTG CGCTGGGGCG
 GTGCTTTGGC TGAACCGACA CCGGTGGCGC GCGGCGGGCG CGACCGACAC GCGACCCCGC

2821 CTGGTGCTCG CGGGTGCTT CTTTCTCCTC GGCTTCCTCT TCGGTAGGGG GCGGCTCGC
 GACCACGACC GCCCACCGAA GAAAGAGGAG CCGAAGGAGA AGCCATCCCC CCGCGAGCG

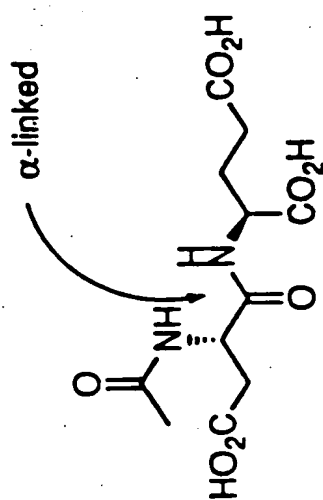
2881 GCAGCAAACC TCGGAGTCTT CCCCCTGGTG CCGCGGTGCT GGGACTCGCG GGTGAGCTGC
 CCTCGTTTGG AGCCTCAGAA CGGGCACCAC GCGGCCACGA CCTGAGCGC CCACTGAGC

2941 CGAGTGGGAT CCTGTTGCTG GTCTTCCCCA GGGGCGGGCA TTAGGGTCCG GGTAAATGTG
 GCTCACCTA GACAACGAC CAGAAGGGGT CCCCAGCGCT AATCCAGCC CCATTACAC

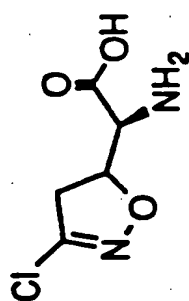
3001 GGTGAGCACC CCTCAG
 CCACTCGTGG GGAGCTC

90/130

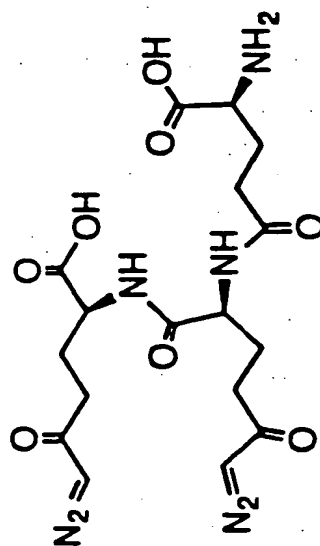
FIG. 59



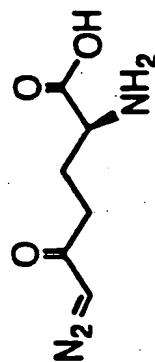
NAAG 1
N-acetyl-L-glutamate



Acividin



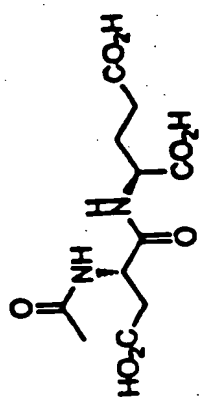
Azotomycin, becomes active by *in vivo* conversion to DON



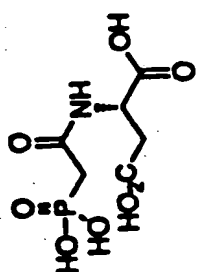
6-diazo-5-oxo-norleucine, DON

91/130

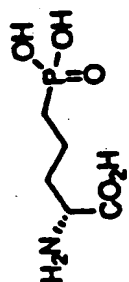
FIG. 60



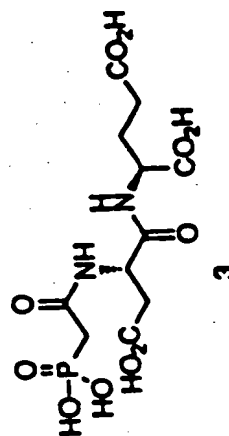
NAAG ¹
N-acetylaspartyl-L-glutamate



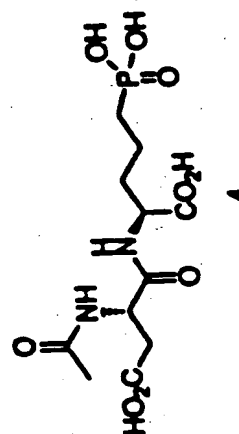
PALA ²
N-phosphonoacetyl-L-aspartate



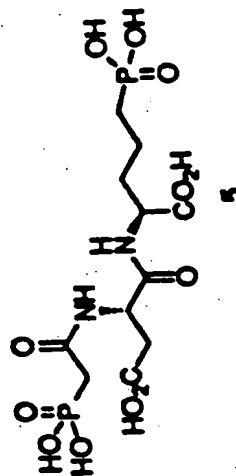
D-APV
L-Glu antagonist



3

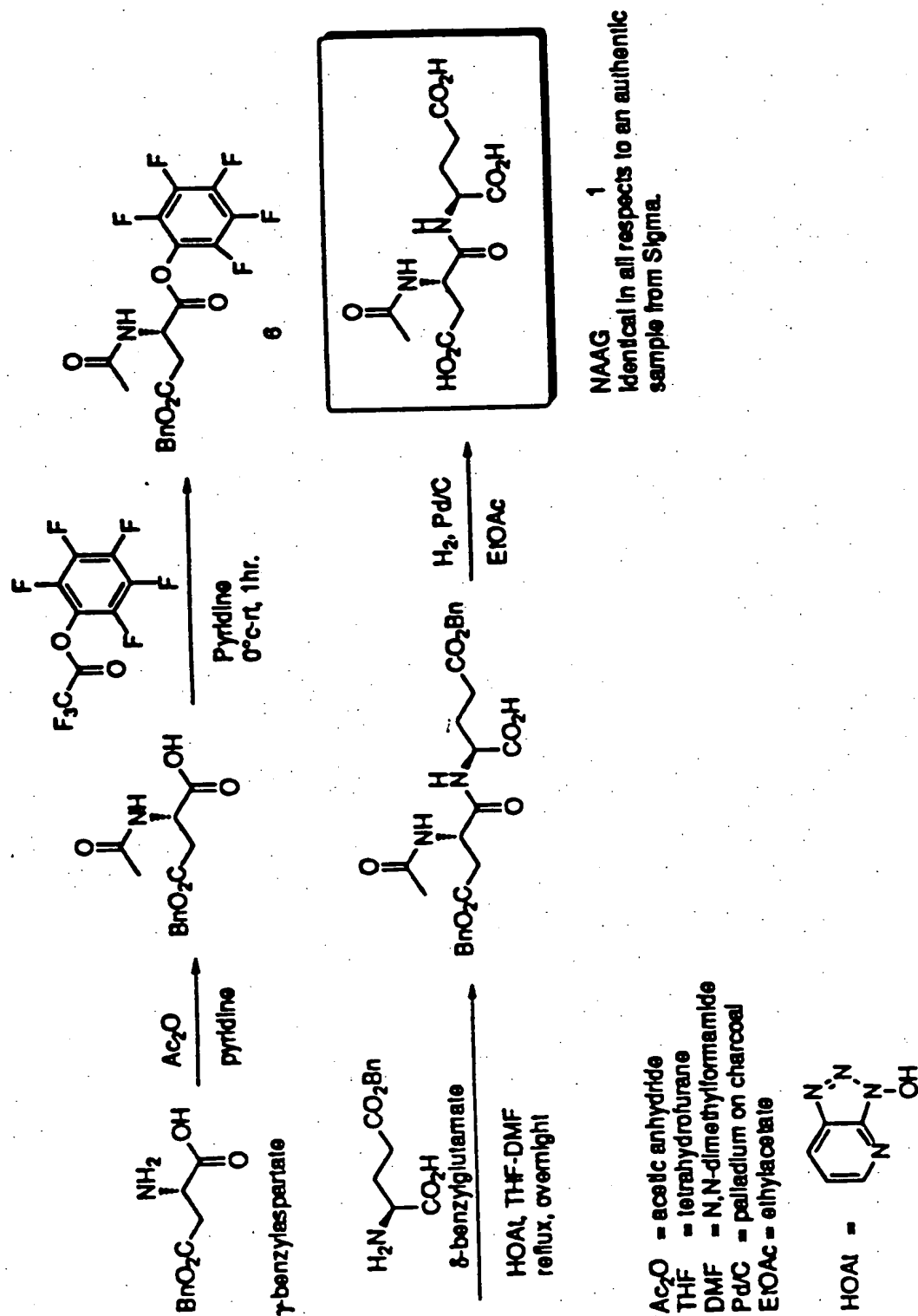


4



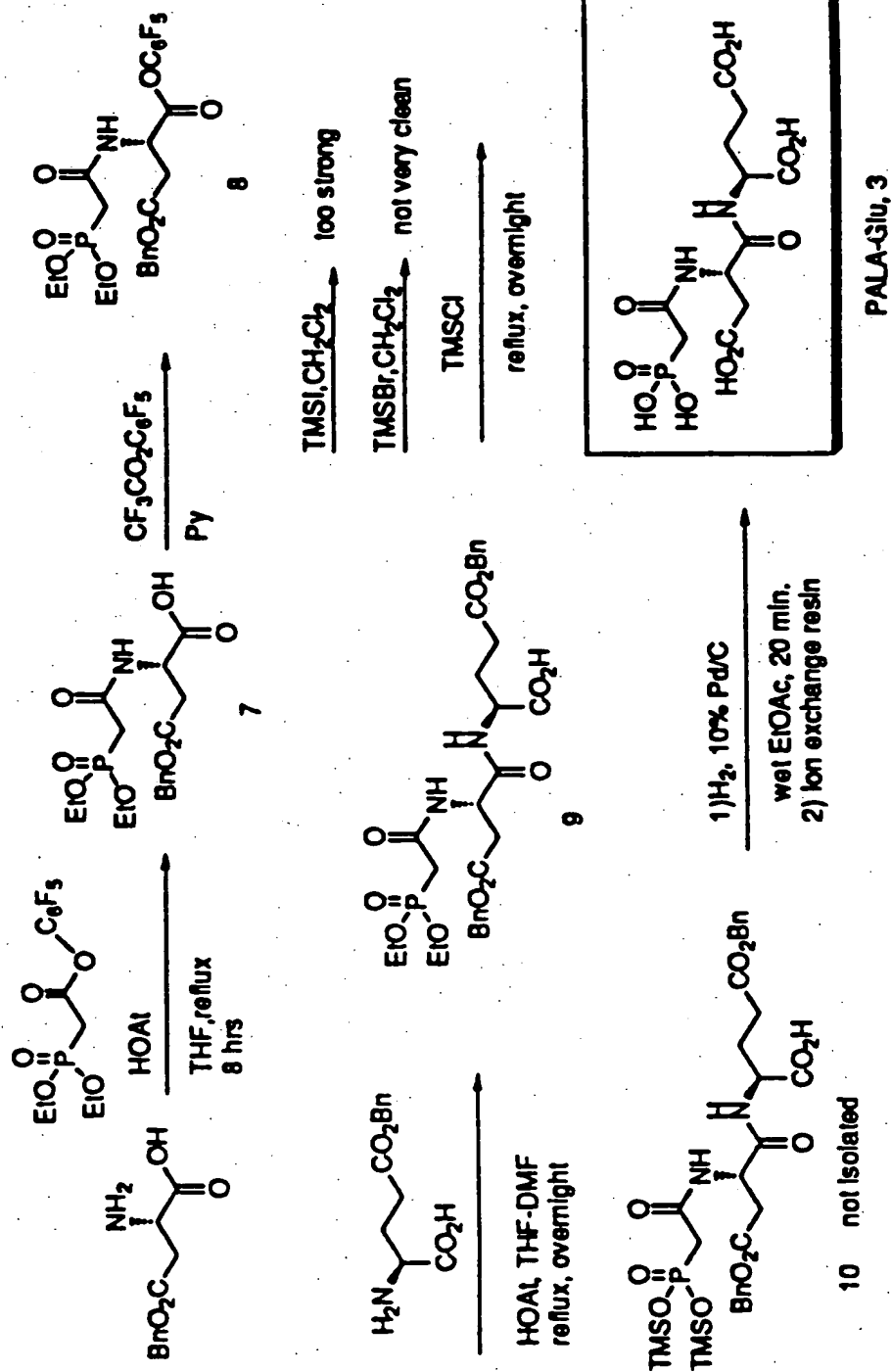
5

FIG. 61



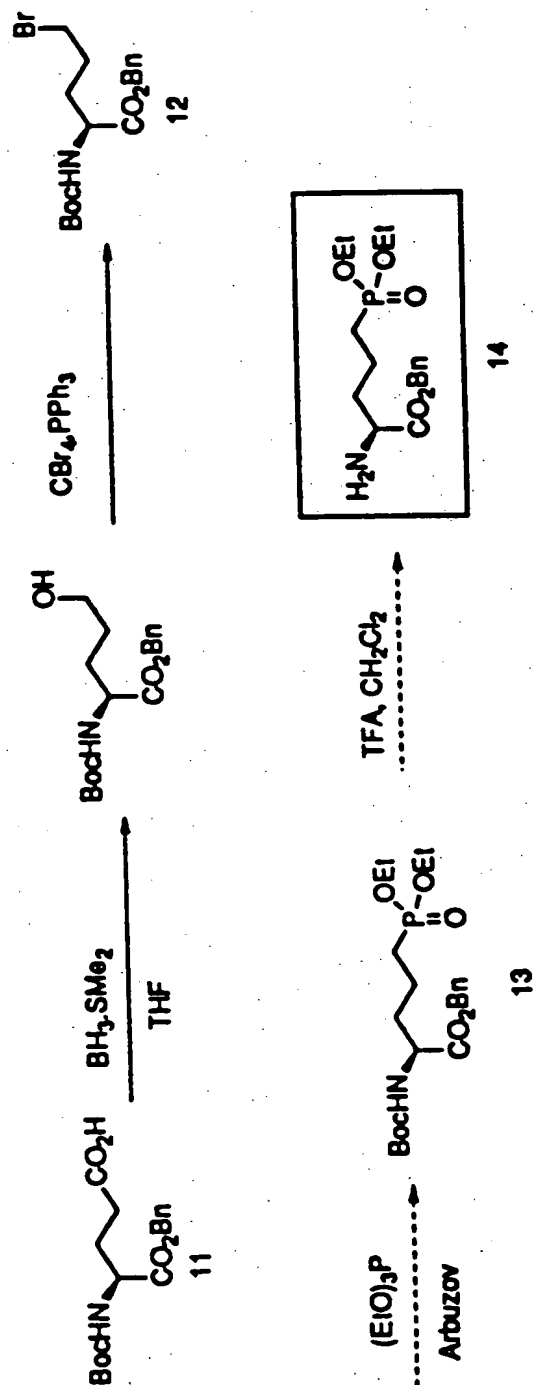
93/130

FIG. 62



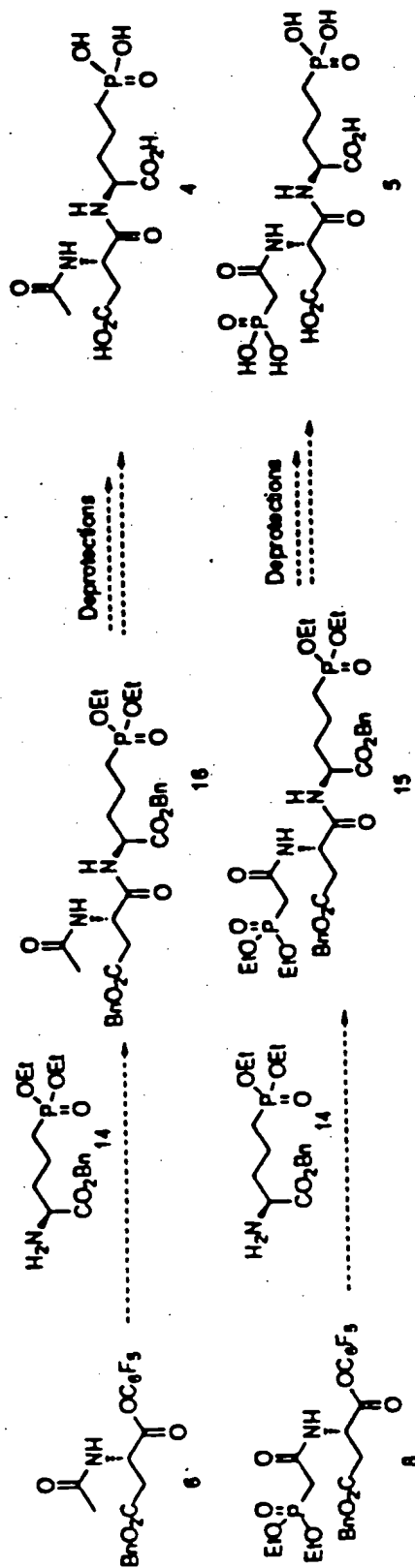
94/130

FIG. 63



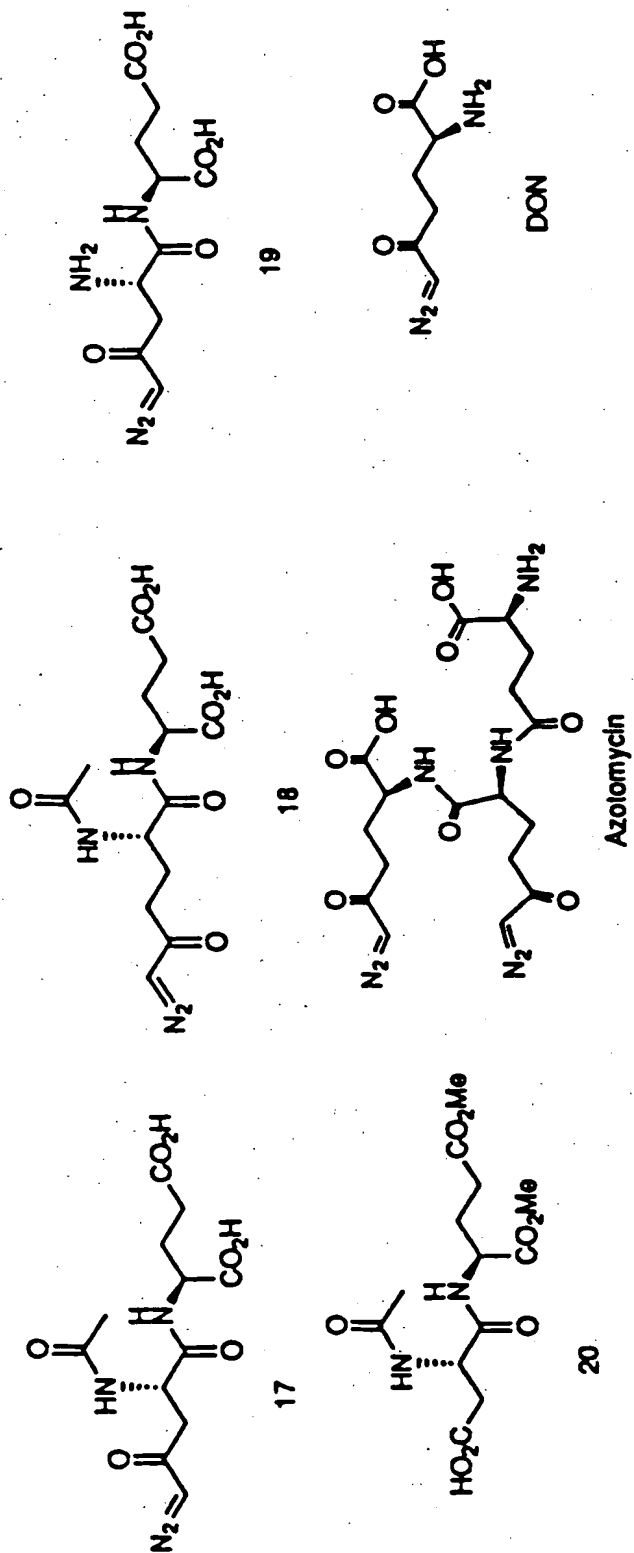
95/130

FIG. 64



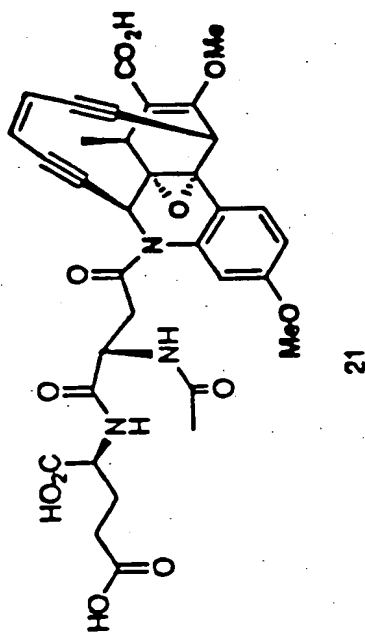
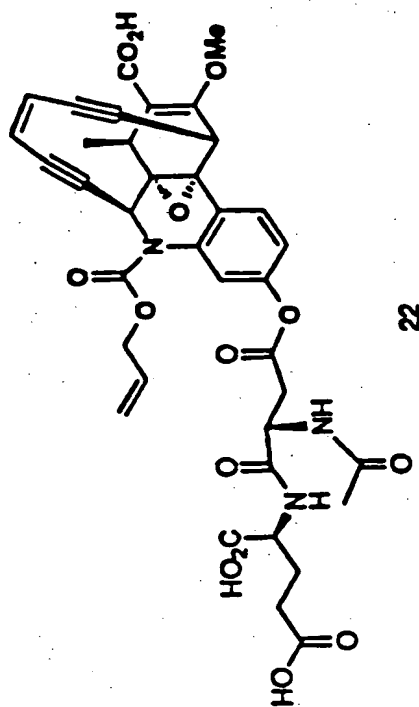
96/130

FIG. 65

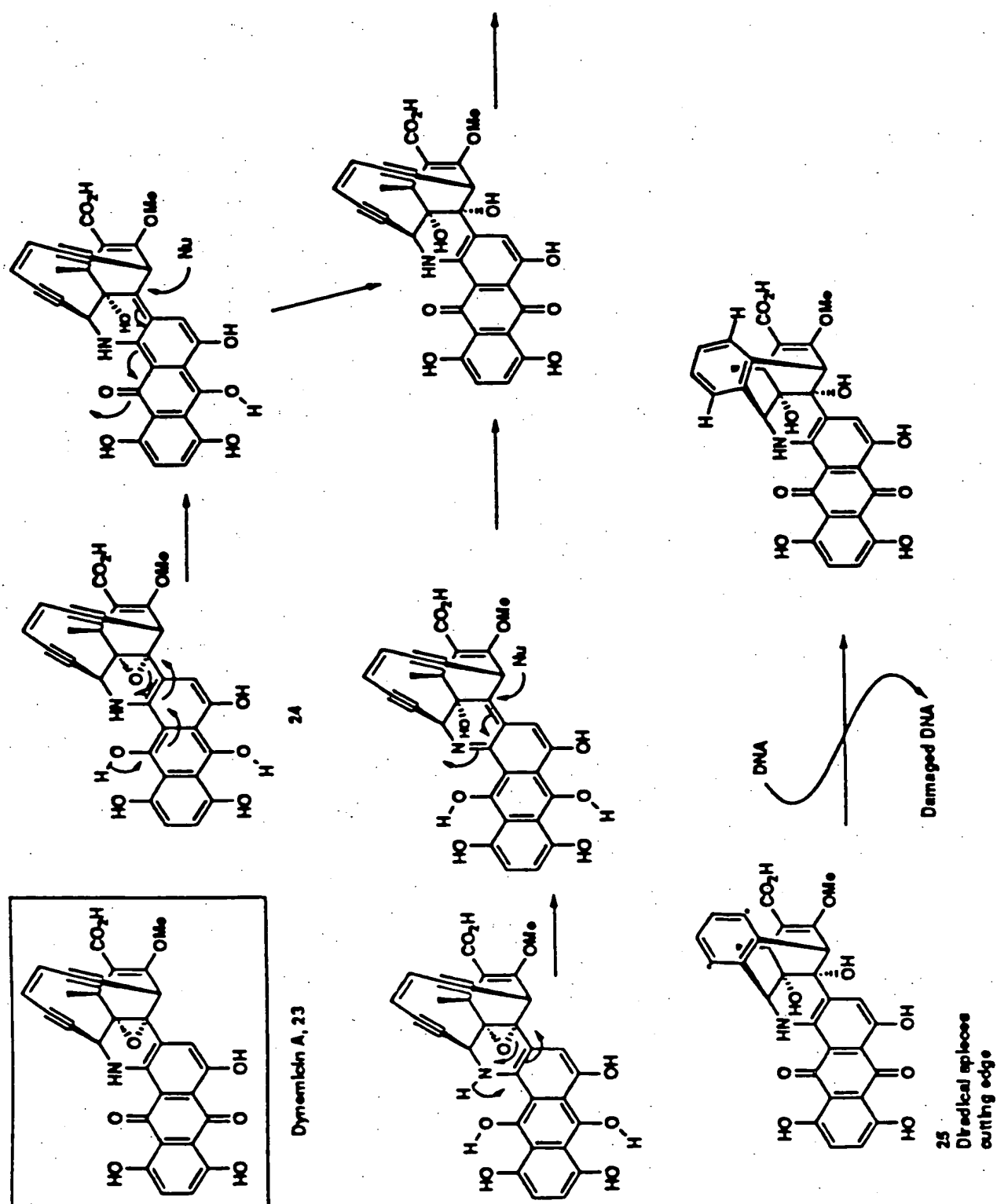


97/130

FIG. 66

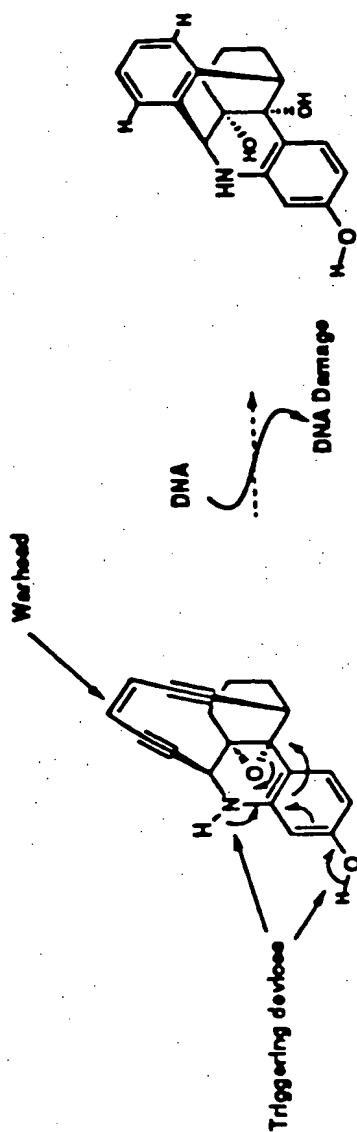


98/130

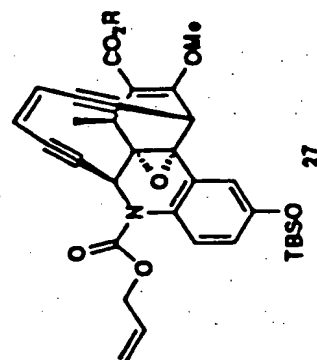
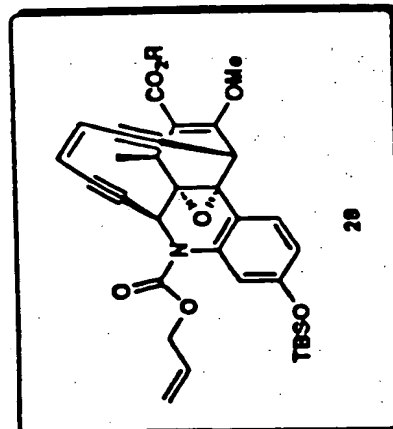


99/130

FIG. 68

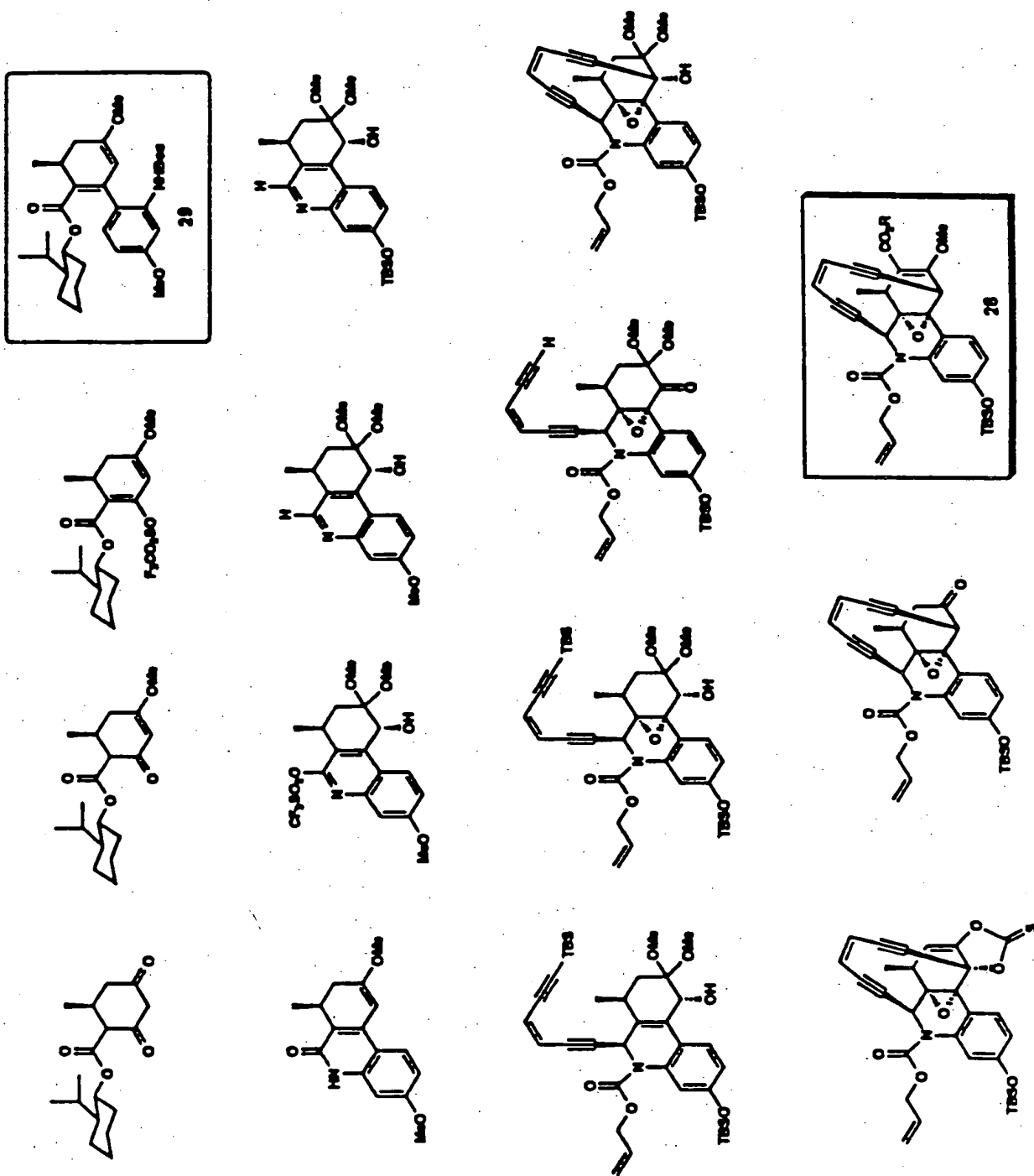


26
active at the nano to picomolar levels in different cell lines
readily rearranges when one or both
triggering devices are deprotected



100/130

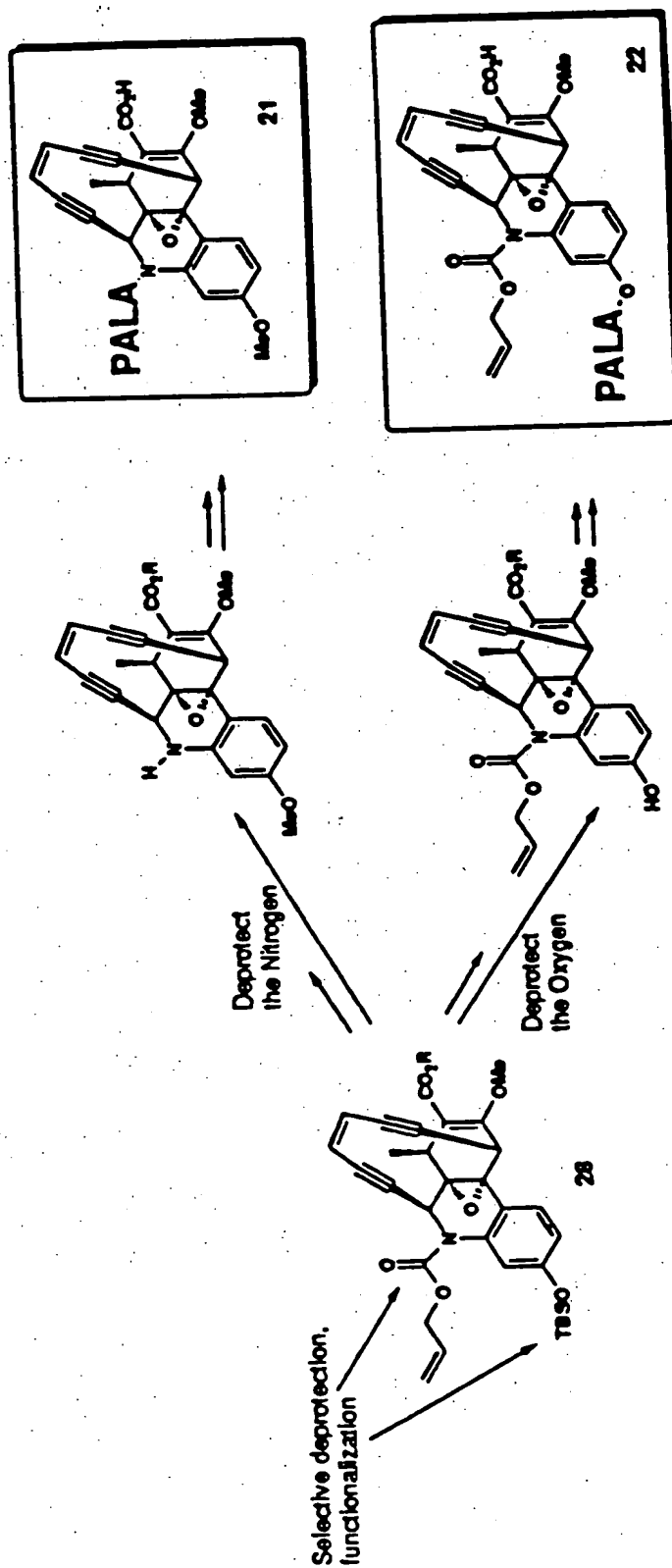
FIG. 69



17 Steps for the optically active form 2

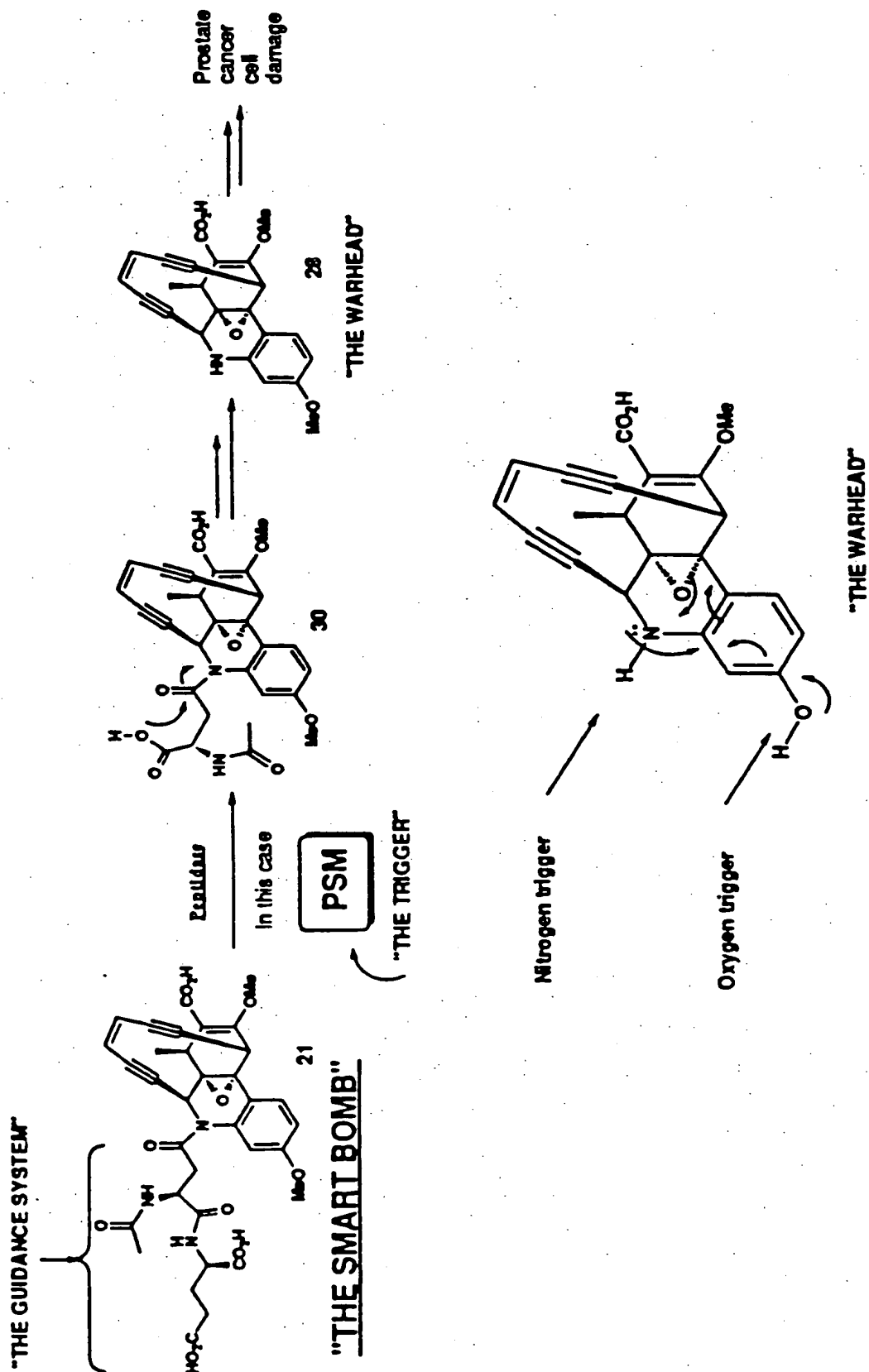
101/130

FIG. 70



102/130

FIG. 71



103/130

FIG. 72A

1 TAGGGGGCG CCTCGGGAG AACCTCGA GTCTCCCCG TGGTCCGCG GTGCTGGGAC
NTCCCCCGG GGAGGCGTC TTGGAGCCT CAGAAAGGGC ACCACGGGCG CACGACCCCTG

61 TCGCGGGTCA GCTGCCGAGT GGGATCCTGT TGCTGGTCTT CCCCAGGGGC GCGGATTAGG
AGCGCCAGT CGACGGCTCA CCTAGGACA ACGACCAGAA GGGGTCCCCG CCGCTAATCC

121 GTCGGGGTAA TGTGGGCTGA GCACCCCTCG AGTTAGGAGG AGGTAGCTG GGAACGGTGC
CAGCCCCATT ACACCCCACT CGTGGGAGC TCAATCCTCC TCCATCGAC CCTTGCCAG

181 AGGGCTGAGT TCTCGACAAG CTGCTGGTAG GACAGTCACT CAGGTTGAGG GTAGAAGTGA
TCCCGACTCA AGAGCTGTTT CAGCACCATC CTGTCAGTGA GTCCAAGTCC CATCTTGACT

241 GAGAACCTGA AACTGGGCGT AGAAGGTC CAAGTGCTGG AGCCCTGCAA GACAGAGGAA
CTCTTGACT TTGACCCGCA TCCTTCCAG GTTCACGACC TCGGAGCGTT CTGTCTCCTT

301 GTTTTTTTT TGCTTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TGTGTTGT
CAAAAAAAA ACGAAAACAA ACAAACAA AACAAAACAA ACAAACAA ACAAACAA

361 TTTTTTTACC TCTCTGTGCA TTCTTTCTT CTGGAAGTA ACAGAGGCAA GCTTGGGAAC
AAAAAATGG AGAGACACGT AAGAAAGAG GAACCTTCAT TGTCTCCGTT CGAACCCCTG

421 TGTGTGAACC AGGTCAGCAA TCTGGACAGG TCTTTACCAG CCGGTCTTTT GCTGTTTTC
ACACACTGG TCCAGTCGTT AGACCTGTCC AGAATGGTC GCCCAGNAAA CGACAAAAG

481 CTGGGTACTG ATTTGCAGAC TTGATCCAAC TTTCTAAGAA AAGCAGAACC ACACAGGCAA
GACCCATGAC TAAACGTCTG AACTAGGTTG AAGATTCTT TTCGTCTTGG TGTGTCGGTT

541 GCTCAGACTC TTTTATTAAA TTCCAGTTT GACTTTGCCA CTTCTTAGTG GCCTTGAACA
CGAGTCTGAG AAAATAATT AAGGTCAAAA CTGAAACGGT GAAGATCAC CGGAACCTTG

104/130

FIG. 72B

601 AGTTACCGAG TCCCTCTCAG CGTTAGTTAC CCTATTTTAT GATGAGGATA ATATTATCTG
TCAATGGCTC AGGGAGAGTC GCATCAATG GGATAAATA CTACTCCTAT TATAATAGAC

661 CAAATTATTG GTAATAGTAA ATAATATAGC ATGTAAATCT CCTAGCACAG TACTGGGATT
GTTTAATAAC CATTATCATT TATTATATCC TACATTIAGA GGATCGTGTC ATGACCCCTAA

721 TTCGCCACTT TATTCTTCT TTTACCAAGA TACTCCTCAT TGGACTTTAA TACACAGGAC
AAGCGGTGAA ATAAAGAAGA AATCGTTCT ATGAGGAGTA ACCTGAAATT ATGTGTCCCTG

781 TAGTCTAAGG TATCACCAGG TAGTCCACTC CTGCTGGAA TTCTTGACCC TCTTTCGGGA
ATCAGATTCC ATAGTGGTCC ATCAGGTGAG GACGAGCCTT AAGAACTGGG AGAAAGCCCT

841 TTTAGAAGAA TAGGGCATGG ACCAGATGGG TTTAAACAAA TTCAATATCT TCCACTAGCT
AATCTTCTT ATCCCGTACC TGGTCTACCC AAATTGTCTT AAGTTATAGA AGGTGATCGA

901 TCACCTTGGG GTTGTAAAA GATTTTGA A CCACACACTG TGCTCATAA C AATCTTCATC
AGTGGAAACC CAACAATTT CTAAAACTT GGTGTGTGAC ACGAGTATTG TTAGAAGTAG

961 TCTTAAAGG ATTTTATCT TCCTGGTATT GCCCTCACTC TCATCCCTGT ATTCCGTGCT
AGAATTTTCC TAAATAAGA AGGACCATAA CGGGAGTGAG AGTAGGGACA TAAGGCACGA

105/130

FIG. 72C

1021 CAGTGGCTGA CACAGAAGAG TTCTTTATTG ATGTCGGCCC CCCACCCACT AGGATTCTCT
GTCACCGACT GTGTCTTCTC AAGAAATAAC TACAGGGCGG GGTGGGTGA TCCTAAGAGA

1081 GCTCTCCCTT CCCCTACAG GCCTCCATCC TCTTCATCCT GTTCATTTT CAGATCTCAG
CGAGAGGGGA GGGGATGTC CGGAGGTAGG AGAAGTAGGA CAAGTAAAAA GTCTAGAGTC

1141 TTCAAGCATC TCGTCTCAG TGTGGTGTTT CCTGATCCCT CACTCTAATC CAAGTCTTTC
AAGTTCGTAG AGCAGGAGTC ACACCACAAA GGAAGTAGGA GTGAGATTAG GTTCAGAAAG

1201 TGTTTTATGC ACAGGTGGAA TCTTATTTC GTTGGCTCC AATCATGTAT TTAAATAAGC
ACAAATACG TGTCCACCTT AGAATAAAG CAAACGCAGG TTAGTACATA AAATTATACG

1261 ATGTATATAT GTATGTGCAT TTGTATGCAT GCGATTAGA ACTAGAATAA TTAATAATTG
TACATATATA CATAACGTA AACATACGTA CGCTAATTCT TGATCTTATT AATTATTAAAC

1321 GAAAGCTCCA TGAAGCTGG TTGGGGACTA ATTTGTAAAC TACTTTATTC CCAGATCCTG
CTTTCGAGGT ACTTTCGACC ACCCCCTGAT TAAACATTG ATGAATAAAG GGTCTAGGAC

1381 TAATTCTCT AAATAAACCC TGGATCTTG CCTATCTCC TTCAGGTAA AAGCCAACTG
ATTAAAGAGA TTTATTGGG ACCTTAGAAC GGAATAGAGG AAGTCCAATT TTCGGTTGAC

1441 CAAGGTCTAA TGAATGCAGG ATCTAGCTAT CCATTGTTT TGGCCGCCCTA TGGTGCACT
GTTCCAGATT ACTGACGTCC TAGATCGATA GGTAAACAAAG ACCGGCGGAT ACGCACGTGA

1501 GGGTGTCTGG CAGAGAGGCT GGGTAAATG TAGTTTCATT GTAGCTGTCT GACTTGGATT
CCACAGACC GTCTCTCCOA CCCATTAAAC ATCAAAAGTAA CATCGACAGA CTGAACCTAA

1561 TCTCAGCCTT ACTTCACTGG AAACGCAAC TCTCACAGCA TTTTGTTTTA GTTTCAGAAT
AGAGTGGGA TGAAGTGACC TTTGGTTTG AGAGTCTCGT AAAACAAAT CAAAGTCTTA

1621 CAGAGCAAT TAGAAGTCTG AATTCCTTC AACACTTGA AATAATTAT TTATTGAAA
GTCTCGTTTA ATCTTCAGAC TTAAGGGAAG TTGTGAACCT TTATTAAATA AATAAATTT

1681 TATATTCTA ATTAATTCGT TATAAAAATG TATTAAATGC TTATTTGAGT CAGCAGAGGA
ATATAAGTAT TAATTAGCA ATATTTTAC ATAATTAGG AATAAACTCA GTCGTCTCCT

106/130

FIG. 72D

1741 AGATAGAAAC TTTATGAAAG TAGAAGGTGG ATCTCCTTTT TGCCTTCATT TTCAGAACAT
TCTATCTTGG AATACTTTC ATCTTCCACC TAGAGGAAAA ACGGAAGTAA AAGTCTTGTA

1801 CTCGTTTACA CCCATTAGTT GAAACATTAA TGTCAATTTA TTTTCGTCCT GATTATCTCA
GAGCAANTGT GGGTAATCAA CTTTGTAATT ACAGTAAAT AAAAGCAGGA CTAATAGAGT

1861 TAAACATTT CTTAGAAATA CAGCAATACC TATCATTGAA GTTGGATAAG AAATATTTTG
ATTTGTAAA GAATCTTATT GTCGTTATGG ATAGTAACTT CAACCTATT CTTATNAAAC

1921 CAATTGGTTT GCAACTTAAA AATCTGTTTG CATGACTCTT TTTCAGTGAA AGTAGGCAAG
GTTAACCAAA CGTTGAATTT TTAGACAAAAC GTACTGAGAA AAGTCACTT TCATCCGTTT

1981 AGAAATTAAA ATTCAGAAAT ATCTCACCTA ATGTCAGAGG TAATATTGAT AATTGTGTT
TCTTTAATTT TAAGTCTTTA TAGAGTGGAT TACAGTCTCC ATTATAACTA TTAAACACAA

2041 TTACAAATAA TACATACAAC AATAATGAAA AATAAGTCCT ATCTATAGGC TCGTATCTCA
AATGTTTATT ATGTATGTTG TTATTACTTT TTATTCAGGA TAGATATCCG AGCATAGAGT

2101 TGCCTATTTT TGGATGTATT TTTC
ACGGATAAAA ACCTACATAA AAAGT

107/130

FIG. 73A

10 20 30 40 50 60
1 TGAAAAATAC ATCAAAAATA GGCATCAGAT ACGAGCCCTAT AGATAGGACT TATTTTTTAT
ACTTTTTATG TAGTTTTAT CCGTACTCTA TGCTCGGATA TCTATCCTGA ATAAAAAATA
61 TATTGTTGTA TGTATTATTT GTAAACACA AATTATCAAT ATTACCTCTG ACATTAGGTG
ATNACAACAT ACATAATAAA CATTTTGTGT TTAATAGTTA TAATGGAGAC TGTAAATCCAC
121 AGATATTCTG AATTTTAATT TCTCTGCTT TCTTCACTG AAAAGAGTC ATGCAAAACAG
TCTATAAGAC TTAANTTAA AGAGAAGGA TGAAGTGAC TTTTCTCAG TACGTTTGTG
181 ATTTTAAAGT TGCMAACCA TCGCAAAATA TTTTATTATC CAACCTCAAT GATAGGTATT
TAAAAATTCA ACGTTTGGT AACGTTTAT AAAAAATAG GTTGAAGTTA CTATCCATAA
241 GCTGTTAATT CTAAGATATG CATTAAATGT TTCAACTAAT GGGTGTCAA CGAGATGTTT
CGACAATTAA GATTCATATAC GTAATTAACA AAGTTGATTA CCCACAGTTT GCTCTACAG
301 TGAAAATGAA GGCMAAAGG AGATCCACCT TCTACTTTCA TAAAGTTTCT ATCTTCTCT
ACTTTTACTT CCGTTTTTCC TCTAGGTGA AGATGAAAGT ATTTCAAAGA TAGAAGGAGA
361 GCTGACTCAA ATAAGCATTT AATACATTTT ATAACGAATT AATTATGAAT ATATTTCAA
CGACTGAGTT TATTGCTAAA TTATGTAAA TATTGCTTAA TTAATACTTA TATAAAGTTT
421 TAAATAAATT ATTTCCAAGT GTTGAAGGAA ATTCAGACTT CTAATTGCT CTGATTCTGA
ATTATTTAA TAAAGGTCA CAACTTCTT TAAGTCTGA GATTAAACGA GACTAAGACT

108/130

FIG. 73B

481 AACTAAACA AATGCTCTGT GAGAGTTTGC GTTCCAGTG AAGTAGCGTG AGAATCCAA
TTGATTTTGT TTACGAGACA CTCTCAAACG CAAAGGTCAC TTCATCGCAC TCTTAGGTT

541 GTCAGACAGC TACATGAAC TACATTTACC AGCTCTCTGC CAGACACCAG TGCACGATAG
CAGTCTGTGG ATGTACTTTG ATGTAATGG TCGAGAGACG GTCTGTGGTC ACGTGTATC

601 CGCAGACAT GTAGCTAGAT CTCAGTCATA GCTNNNNNNN NNNNNNNNNN AGACCTTGCA
GCGTCTTGTA CATCGATCTA GAGTCAGTAT CGANNNNNNN NNNNNNNNNN TCTGGNACGT

661 GTTGGCTTTT AACCTGAAGG AGATAAGGCA AGATTCCAGG GTTTATTAG AGAATTACA
CAACCGAAAA TTGGACTTCC TCTATTCCGT TCTAAGGTCC CAAATAAATC TCTTTAATGT

721 GGATCTGGGA ATAAAGTAGT TACAAATTA GTCCCAACC AGCTTTCATG GAGCTTTCAA
CCTAGACCCCT TATTTCATCA ATGTTTAAAT CAGGGGTTGG TCGAAAGTAC CTCGAAAGTT

109/130

FIG. 73C

781 TTATTAAATTA TTCTAGTTCT TAATCGGCAIG CATACAATGC ACAIACATAT ATACATGCAT
AATAATTAAT AAGATCAAGA ATTAGCGTAC GTATGTTACG TGTATGTATA TATGTACGTA

841 ATTAATAATAC ATGATGGAC GCAAAACGGAA ATAAGATTCC ACCTGTGCAT AAAACAGAAA
TAATTTTATG TACTAACCTG CGTTGGCCTT TATTCTAAGG TGGACACGTA TTTTGTCTTT

901 GACTTGGTTA GAGTGAGGGA TCAGGAACA CACACTGAG GACGAGATGN NNNNNNNNN
CTGAACCAAT CTCACTCCCT AGTCCCTTGT GGTGTGACTC CTGCTCTACN NNNNNNNNN

961 NTAGTGGGTG GGGGGGGGAC ATCAATAAAG AACTCTTCTG TGTACGCCAC TGAGCACCGA
NATCACCCAC CCCCCGCTG TACTTATTC TTGAGAAAGAC ACAGTCGGTG ACTCGTGCCT

1021 ATAAAGGGAT GAGAGTGAGG GCAANTACCA GAAGATAAA ATCCCTTTAA GAGATGAAGA
TATTTCCTA CTCTCACTCC CGTNNATGTT CTCTTATTT TAGGAAAAT CTCTACTTCT

1081 TTGTTATGAG CACAGTGTTGT GNTTCAAAA ATCTTTTAAAC AACCCCAAGG TGAAGCTAGT
AACAACTACTC GTGTCAACACA CCNAAGTTT TAGAAAATTG TTGGGGTTCC ACTTCGATCA

1141 TGGAAAGATAT TTGAATTGT TTAACCCAT CTGGTCCTAG CCTATTCTT TGAATCCCGA
ACCTTCTATA AACTTAACA AATTGGGTA GACCAGGATC GGGATAAGAA ACITAGGGCT

110/130

FIG. 73D

1201 AAGAGGGTCA AGAATTCCGA GCAGGAGTGG ACTACCTGGT GATACCTTAG ACTAGTCCTG
TTCTCCCACT TCTTAAGGCT COTCCTCACC TGATGGACCA CTATCGAATC TGATCAGGAC

1261 TGTATTAAAG TCCAATGAGG AGTATCTTGG TAAATAATA AATAAGTCC CGAAATCCC
ACATAATTTC AGTTACTCC TCATAGAACC ATTATATTAT TTATTCAGG GCTTTTAGGG

1321 AGTACTGTGC TAGGAGATTI ACATGCTATA TIATTTACTA TNNNNNNNT AATTGCAGA
TCATGACACG ATCCTCTAAA TGTACGATAT AATAAATGAT ANNNNNNNNA TTAAACCTCT

1381 TAATATTATC CTCATCATAA AATAGGGTAA CTAAGCTGA GAGGACTCG GTAACTTCTT
ATTATAATAG GAGTAGTATT TTATCCCATTT GATTGCGACT CTCCTGAGC CATTGAACAA

1441 CAAGGCCACT AAGAAGTGGC AAGTCAAA CTGGAATTTT AATAAAGAG TCTAGCTTGC
GTTCCGGTGA TTCTTCACCG TTTCAGTTT GACCTTAAA TTAATTTCTC AGATCGAAG

1501 CTGTGTGGTT CTGCTTTTCT TAGAAAGTTG GANNAAGTCT CANATCAGTA CCCAGGAAA
GACACACCAA GACGAAAAGA ATCTTTCAC CTNNTTCAGA GTNTAGTCAT GGGTCTTTT

1561 ACAGCAAAAG ACCCGTGGT AAAGACCIGT CCAGATTGCT GACCTGGTTC ACACANHTCC

111/130

FIG. 73E

TGTCGTTTTC TGGGCGACCA TTCTCGGACA GGTCTAACGA CTGGACCAAG TGTGTNNAGG

1621 AAGCTTGCCT CTGTTACTTC CAAGGAAGAA AGAATGCACA GAGAGGTAA AACAACAACA
TTCGAACGGA GACAATGAAG GTTCCTTCTT TCTTACGCT CTCICCATTT TTTTGTTTGT

1681 AACCAACA AACAACAACA AACAAACA AACAAACA AAGCAAAA AACTTCCTC
TTGGTTTGT TTGTTTGT TTGTTTGT TTGTTTGT TTCGTTTTT TTGAAGGAG

1741 TGTCTTGCAG GGCTCCAGCA CTTGGAACCT TCCTACGTCC TANTTTCAGG TTCTCTCAGT
ACAGAACGTC CCGAGGTCGT GAACCTTGA AGGATGCAGG ATNAAGTCC AAGAGAGTCA

1801 TCTACCCCTCA ACCTGAGTGA CTGTCCTACC AGCAGCTTGT CGAGAACTCA GCCCTGCACC
AGATGGGAGT TGGACTCACT GACAGGATGG TCGTCGAACA GCTCTTGAGT CGGACGCTGG

1861 GTTCCCAGCT ACCCTCCTCC TAACTCGAGG GGIGCT
CAAGGGTCCA TGGGAGGAGG ATTGAGCTCC CCACGA

112/130

FIG. 74A

1 GGATTCGTGTT GAGCCCTAGC TCATTATGAT GTCCTGTTGT CCTACCCAAA TAAGACTCAT
CCTAAGACAA CTCGGGATCG AGTAATACTA CAGGACAACA GGAATGGGTTT ATTCTGAGTA

61 CCCAACTACA TCTCAATAAT TAATGAAGAT GGAATGAGG TAAATAATTA ATAAATAAAT
GGGTGATGT AGAGTTATTA ATTACTCTA CCTTACTCC ATTTTATT TATTATTATTA

121 AAAAGAMACA TTCCCCCCA TTTATTATTT TTTCAAATAC CTTCATGAA ATAATGTTCT
TTTCTTTTGT AAGGGGGGT AATAATAAA AAAGTTATG GAAGTACTT TATTACAAAG

181 ATCCCTCTCT AATATTAAAT AGAATCAAT ATTATTGGAA CTGTGAATAC CTTAAATATC
TAGGGAGAGA TTTATAATTA TCTTAGTTA TAATAACCTT GACACTTATG GAAATTATAG

241 TCATTATCCG GTGTCAACIA CTTTCCTATG ATGTTGAGTT ACTGGGTTA GAAGTCGGGA
AGTAATAGSC CACAGTTGAT GAAAGCATAC TACAACCTCA TGACCCCAAT CTCAGGCCCT

301 AATAATGCTG TAAANNNNN AGTTAGTCTA CACACCAATA TCAATAATGA TATACTTGTA
TTATTACGAC ATTTNNNNN TCAATCAGAT GTGTGTTAT AGTTTATCT ATATGAACAT

361 AACCTCCAAG CATAAAAGA GATACTTAT AAAGAGGTT CTTTTTCT TTTTTTTT
TTGGAGGTTT GTATTTTCT CTATGAAATA TTTCTCCAA GAAAAAAGA AAAAAAAA

113/130

FIG. 74B

421 TCCAGATGGA GTTTCACCTCC TGTCAGGCCAG GCNGAGTGCA GTGGTGCCAT CTCGGCTCAC
AGGTCTACCT CAAAGTGAGG ACAGTCCGTC CGNCTCAGGT CACCACGGTA GAGCCGAGTG

481 TGC AACCTCC ACCTCCCATG TTCAAGGGAT TCTCCTTCT CAGTCTCCTG AGTAGCTGGG
ACGTTGGAGG TGGAGGGTAC AGTTCCTTA AGAGGAGGA GTCAGAGGAC TCATCGACCC

541 ATTACAGGTG TGCACCAACA CACCCAGCTA ATTTTGTAT TTTTAATAGA GACAGGGTTT
TAATGTCCAC ACGTGTGTGT GTGGGTGGAT TAAAAACATA AAATTATCT CTGTCCCAAA

601 CATCGATGTT GCCCAGGCTA GTCTCGAACT CCTGACCTCT AGGIGATCCA CCCGCTCAG
GTAGCTACAA CCGGTCCGAT CAGAOCCTGA GGA CTGGAGA TCCACTAGGT GGGCGGAGTC

661 CCTCCCAAG TTGTAGAAIT ACACGTGTGA GGCACGTCTC TGGCCAGGAG ATACATTTTT
GGAGGGTTTC AACATCTTAA TGTGCACACT CCGTGACGAG ACCGCTCCTC TATGTAAAAA

721 GATAGGTTTA ATTTATAAG AACTGCACA GATTTCGACT TCTGGGAAA TCACGATCCA
CTATCCAAAT TAAATATTTC TGTGACGTGT CTAAACCTCA ACCACCTTT AGTGCTAGGT

114/130

FIG. 74C

781 GTATGCCATTT GACCCAGCAA TTTTATTGG TACTTAATGA TTATATCTCA ATTGATCAGG
CATACGTAAA CTGGGTCGTT AAAAATAACC ATGAATTACT AATATAAGT TAACTAGTCC

841 TTGAACCTCG TGGGAGAAAT TTGTGTGTTG ACATTTGAGA GGACAGTTTG GAGGCAAGGT
AACTTGAGAC ACGCTTCITA AACACACACC TGTAACCTCT CCGTCAAAAC CTCGGTTCCA

901 ATTTTAGTAG ATTAAAGAA TTTGAATCTT GTTGCAGT TGGGCATAT ACTGAGAAAG
TAAANTCATC TAAATTCTT AAACCTTAGA CAAACGTTCA ACCCGTATA TGACTCTTTC

961 AGAAGACAAT GCAGATAAAT TGATATATTT ATTATGATGT ATGTTCAATA TGAAGATCA
TCCTCTGTTA CGTCTATTTA ACTATATAAA TAATACTACA TACAAGTTAT ACTTCTTAOT

1021 CAAATATATA CATACATNNA TCTTACTTAA CATACCTCAG TTTTASAGCT ACCGTATGTA
GTTTATATTT GTATGTANNT AGAATGAATT GTATGGAGTC AAATCTCGA TGGCATACAT

1081 GAAGAGTCCA TTTCTATTTA GGTNAGTTCC TTTAGTCCTT TTATTACTGG GCACTCTTAA
CTTCTCAGGT AAAGATTAAT CCATTCAAGG AAATCAGGAA AATTAIGACC CGTGAGAATT

1141 TTACATGTAG CTTGAATAT GTCCAGTTTG AGCAGTGAAC TGAATATGTC ATGTGATTAA
AATGTACATC GAACTTTATA CAGGTCAAAC TCGTCACCTG ACTTTTACAG TACACTAATT

1201 GTACATATAT AATTTTTTTT CATAGTAGGT CAATAACCTC CTTTATTGA CTAAATGATC
CATGTATATA TTAAAAAAA GTAATATCCA GTTATTGGAG GAAATATACT GATTACTTAG

1261 AGTCTCTAA TGATTATACG
TCAAGAGATT ACTAATATOC

115/130

FIG. 75A

10 20 30 40 50 60
1 AATCAAAATA AACAGTTAA AGTTTGATTA CTATAATCAA ACACAAAATA AATGAATATT
TTAGTTTAT TTTGTCAATT TCAAACTAAT GATATTAGTT TGTGTTTTT TTACTTATAA
61 ATCTTTTATG TCAGTAGAGG GTGATGAAT CCTCAGGAT TTGATGATA GTATCAGATA
TAGAAATAC AGTCATCTCC CACTTACTTA GGAAGTCCTA AAACACTAT CATAGTCTAT
121 CCCAGCACTA TGCTAGAAGT TGTGAAGAT TCACGAGATG AATAATCAC AGATTCTGTC
GGGTCGTGAT ACGATCTTCA ACACCTCTTA AGTCTCTAC TTATTTAGTG TCTAAGACAG
181 CTCAAAATGG TTAGATCTAT TCAGGAACA AAGCTAAAA AACCCACCA ATAACTAAAA
GAGTTTACC AATCTAGATA AGTCCTTGT TTCGATTTT TTGGGGTGGT TATTGATTTT
241 ATCAACCAAA TGAAAAACA CAATCATAA ATAAGTAAGT ACCTATAGAA AGAAAGCTC
TAGTTGGTTT ACTTTTGT GITAGTATT TATTCATTCA TGGATATCTT TCTTTTCGAG
301 AGAGGAGGTA AAAAGATAAC TCTTCCAAA GGAATACTAT ATACTGTAAG CTGTGTACTG
TCTCCTCCAT TTTTCTATIG AGAAGGTTT CCTTATGATA TATGACATTT GACACATGAC
361 ATAGAAGGAA GAATTAGAAA NNNNNNTG TAAGTGGCAT ACATACTAAG CTAOTGTGAA
TATCTTCCCTT CTTAATCTTT NNNNNNNAC ATTACCCGTA TGTATGATTC GATCACACTT

116/130

FIG. 75B

421 CACAAGCCTA AATATGTAGT TGCTTCACAG AAGTTAGAA GTAAATTAAC CTCATGAATT
GTGTTGGAT TTATACATCA ACGAAGTGC TTCCAATCTT CATTTAATTG GAGTACTTAA

481 TCTTGAGAGA ACTTGTAAGG ACTAAGCTTT CGATTTTGGG GAAAGATTTT AATACCAAAAT
AGAACTCTCT TGAACATTCG GATTTCGAAA GCATAAACCT CTTTCTAATA TTATGGTTTA

541 AAAAAGTACC TTTGTTTGGT AATCTCAATC ATTATAATAG TGCTTAGATA ATACCTAGGA
TTTTTCATGG AAACAAACCA TTAGAGTTAG TAATATTATC ACGAATCTAT TATGGATCCT

601 ACAAAATTAA TATTAAATTT ACTTTAAAAA AAAGTACAAG ATTGGGGAAT CACAAGTGGC
TGTTTAATTT ATAATTAAA TGAAATTTTT TTTCATGTAC TAACCCCTTA GTGTTGACCG

661 CTTACTAGAT TCTCTNNNNN NATATGCACT GAAAGAATG AAAAACACTG AACCAATAT
GAATGATCTA AGAGANNNNN NTATACGTGA CTTTCTTAC TTTTGTGAC TTGGTTTATA

721 NIGTTTTTTT AAGTTTAAAA TTAAATTGGA AAAAATAGT AAGGAATATC AGAAGCAAAA
NACAAAAAAA TTCAAATTTT AATTAACTT TTTTATATCA TTCCTTATAG TCTTCGTTTT

117/130

FIG. 75C

781 AAATAAAATG AAAGCAAGAA TCCTCAGAGG TAGCAGGAAA TTGGCTTTG CTTAGATGGA
TTTATTTTAC TTTCGTTCTT AGGAGTCTCC ATCGTGCTTT AAACCGAAAC GAATCTACCT

841 TCTATCAAG CTATGGCCCA TGAAAAGGAT TCAGGAGTTA GTTTAAAGCT GGTTCACATA
AGATAGTTTC GATACCGGGT ACTTTTCTA AGTCCTCAAT CAAATTTCGA CCAAGTGTAT

901 ATGGAATCTA GCAGAAAGCT GTGCATAAAG GTGGTCTAAG AACAAACATA TCCTGACCCAG
TACCTTAGAT CGTCTTCTGA CAGGTATTTC CACCAGATTTC TTGTTGTTAT AGGACTGGTC

961 GTGAGGGGCG TCACNCTNAA TNCCAGCACT TTGGGAGCCC AAGGTGGGTG GATCAGGAGG
CACTCCCCCG AGTNGANTT ANGTCGTGA AACCTCGGG TTCCACCCAC CTAGTGCTCC

1021 TCAGGAGTTT GAGACCAGCC TGACCAACAT GGTGAACCG CGTCTCTACT AAAAATAGAA
AGTCCTCAAA CTCTGGTCGG ACTGGTTGTA CCACTTTGGC GCAGAGATGA TTTTATCTTT

1081 AAATTAGCCG NGCCTACGTG CTTCTAATCC CAGCTGAACT CAGGAGACTG AGACAGGAGA
TTTAATCGGC NCGGATGCAC GAAGATTAGG GTCGACTTGA GTCCTCTGAC TCTGTCCTCT

1141 ATCACTTGAA CCCAGCATGC AAGCTTNNNN NNGCCACTGC ACTCCAGCCT AGGGTGCAAA
TAGTGAACCT GGGTCGTACG TTCGAANNNN NNCGGTGACG TGAGGTCCGA TCCACGTTT

1201 AAAAAAANA ANGACACATT ACTCAGGTAA GGTAATCAAT AA
TTTTTTTTT TNCGTGTAA TGAGTCCATT CCATTAGTAA TT

FIG. 76A

- AAGGTA AAAAATTATCTCTTTTTTTCTCTCCCCCAATGTAAAAAGTTATAG -
- AAGGTA AAAAATTATCTCTTTTTTTCTCTCCCCCAATGTAAAAAGTTATAG -
- TGGGTTTTACATGTGTAGAATCATTTTCTTAAAACTTTATGAATACCATT -
- TGGGTTTTACATGTGTAGAATCATTTTCTTAAAACTTTATGAATACCATT -
- ATTTTCTTGTAATTCTGTGACATGCCACCTTACAGAGAGGACACATTTAC -
- ATTTTCTTGTAATTCTGTGACATGCCACCTTACAGAGAGGACACATTTAC -
- TAGGTTATATCCCGGGGTAAATTGAGCATTGGAATTTGGCCAGTGTAG -
- TAGGTTATATCCCGGGGTAAATTGAGCATTGGAATTTGGCCAGTGTAG -
- ATGTTTAGAGTGAACAGAACAAATTTTTCTGTGCTTACAGGTTATGGCTG -
- ATGTTTAGAGTGAACAGAACAAATTTTTCTGTGCTTACAGGTTATGGCTG -
- TGGCCTACAAGAAGCATGCACTGGGTTTATTATTAACTTTCA GTATCTTT -
- TGGCCTACAAGAAGCATGCACTGGGTTTATTATTAACTTTCA GTATCTTT -
- GTTTTAAATATTTTCTACAAAAATGTTTACTAAATTAAATTG TAGTATGA -
- GTTTTAAATATTTTCTACAAAAATGTTTACTAAATTAAATTG TAGTATGA -
- ATTGTTATAAATAATGAGGGAAAA CAATTTACACATAGCAAATTTAAAAA -
- ATTGTTATAAATAATGAGGGAAAA CAATTTACACATAGCAAATTTAAAAA -
- TTACTGTCATTTGATTTGTTAATATATTTTTCTCTTTAGTGGGAAATTAA -
- TTACTGTCATTTGATTTGTTAATATATTTTTCTCTTTAGTGGGAAATTAA -
- ATTTTAAAAAATTCCCTTTGACTGTAGAACAAATAGGAATTTGGCCTGT -

119/130

FIG. 76B

|||||
- ATTTTAAAAAATTCCCTTTGCGACTGTAGAACAAATAGGAATTTGGCCTGT -
|||||
- GGGGTCTACTTGCTTATTATATTTGTAAGCTAGTGGTAGGAAATAGCAA -
|||||
- GGGGTCTACTTGCTTATTATATTTGTAAGCTAGTGGTAGGAAATAGCAA -
|||||
- TGCTCACTACCACTAATAAGAACATTTCTAAATCTGATGTTCTGAGGATT -
|||||
- TGCTCACTACCACTAATAAGAACATTTCTAAATCTGATGTTCTGAGGATT -
|||||
- TTTAGAGCTTATAGTAGCAAAAAGAAAAGGGAAATTCTATCCGAGATGTC -
|||||
- TTTAGAGCTTATAGTAGCAAAAAGAAAAGGGAAATTCTATCCGAGATGTC -
|||||
- CTTTGTTGTAGGCCTAATGAGAAAAGGTTGAAGATAAAGTTCTGGTACTC -
|||||
- CTTTGTTGTAGGCCTAATGAGAAAAGGTTGAAGATAAAGTTCTGGTACTC -
|||||
- ATTTAAGTGTAATATTGAAAATTGATATTACCGAATCTGGAACAACCAAT -
|||||
- ATTTAAGTGTAATATTGAAAATTGATATTACCGAATCTGGAACAACCAAT -
|||||
- TTAAAATAAGGAAAGAAAGACACTGTGTTTTCT -
|||||
- TTAAAATAAGGAAAGAAAGACACTGTGTTTTCT -

120/130

FIG. 77A

10 20 30 40 50 60
1 AGAAAACACA GTGCTTTCT TCCCTTAATT TAAATTGGTT GTTCCAGATT CGGTAATATC
TCCTTTGTGT CACAGAAAGA AAGGAATAAA ATTAAACCAA CAAGGTCTAA GCCATTATAG
61 AATTTCAAT ATTACACTTA AATGAGTACC AGAAGCTTAT CTTCACCCCTT TTCTCATTAG
TTAAAAGTTA TAATGTGAAT TTACTCATGG TCTTGAATA GAAGTTGGAA AAGAGTAATC
121 GCCTACAACA AAGGACATCT CGATAGAAAT TTCCCTTTTC TTTTGGCTAC TATAAGCTCT
CGGATGTTGT TTCCTGTAGA GCCTATCTTA AAGGGAAGA AAAAACGATG ATATTCCGAGA
181 AAAATCCTC AGAACATCAG ATTAGAAAT GTTCTTATTA GTGGTAGTGA GCATTGGCTA
TTTTTAGGAG TCCTGTAGTC TAAATCTTTA CAAGAATAAT CACCATCACT CGTAAACGAT
241 TTTCCTACCA CTAGCTTACA AATATAATAA GCAAGTAGAC CCCACAGGCC AATTCCTAT
AAAGGATGGT GATCGAATGT TTATATTATT CGTTCATCTG GGGTGTCCGG TTAAAGGATA
301 TTGTTCTACA GTCGAAAGGG AATTTTTTAA AATTTAATTT CCCACTAAAG AGAAAATAT
AACAAAGATGT CAGCTTTCCC TTAAAAAATT TTAATAATAA GGOTGATTTC TCTTTTATA
361 ATTAACAAAT CAAATGACAG TAATTTTTAA ATTGCTATG TGTAAANTGT TTTCCCTCAT
TAATTGTTTA GTTTACTGTC ATTAAAAATT TAAACGATAC ACATTTAACA AAAGGGAGTA
421 TATTATAAC AATTCATACT ACAATTTAAT TTAGTAACA TTTTGTAGA AAATATTTAA
ATAAATATTG TTAAGTATGA TGTAAANTTA AATCAATTGT AAAACATCT TTTATAAATT

121/130

FIG. 77B

481 AACAAAGATA CTGAAAGTTA ATATNAAACC CAGTGCATGC TTCITGTAGG CCACAGCCAT
TTGTTTCTAT GACTTTCAAT TATANTTTGG GTCACGTACG AAGRACATCC GGTGTCGGTA

541 AACCTGTAAG CACAGAAJAA TTTGTTCTGT TACTCTNAAAC ATCTACACIG GCCAAATTCC
TTGGACATTC GTGTCTTTT AAACAAGACA ATGAGATTGG TAGATGTGAC CGGTTTAAAGG

601 AATGCTCGAA TTTAAACCCG GGATAAACC TAGTAATGT GTCCTCTCTG TAAGGTGGGC
TTACGAGCTT AAATTGGGGC CCTATATTGG ATCAITTACA CAGGAGAGAC ATTCCACCCG

661 ATGTCACAGA ATACAAGAA ATAATGGTAT TCATNAAAGTT TTAAGNAAAT GATTCTACAC
TACAGTGTCT TATGTTCTT TATTACCATA AGTAITTCAA AATCTTTTA CTAAGATGTG

721 ATGTAAACC CACTATAACT TTTTACATTG GGGGAGAGAA AAAAGAGAT AATTTTACC
TACATTTTGG GTGATATTGA AAAATGIAAC CCCCTCTCTT TTTTCTCTA TTAATAATGG

781 TT
AA

122/130

FIG. 78A

10	1	GATGCTATTT	GCGCAATTTC	TTATTGACAG	TTTTGAAATG	TTAGGCTTTT	ATCTCCATTT
		CTACGATAAA	CCCGTTAAAG	AATAACTGTC	AAACITTAC	AATCCGAAAA	TAGAGGTAAA
20							
30							
40							
50							
60							
	61	TTTAGTACTT	AAATTTTCCA	ACATGGGTGT	TGCTTGTAT	TTATCAGTA	TAAATAGAA
		AAATCATGAA	TTTAAAGGT	TGTACCCACA	ACGAACAATA	AAATAGTCAT	ATTTATCTT
	121	GAGTGGTTCT	GTTCTGGAAT	TTAGTATATA	CATGAGTATC	TAGTGATGT	CAGCCATGAA
		CTCACCAAGA	CAAGACCTTA	AATCATATAT	GIACTCATAG	ATCACATACA	GTCGGTACTT
	181	AATGAACCTT	TCAGATGTTT	AACCTCAGGG	AACCTAATTG	AGTCATTGCT	CCAGACATTG
		TTACTTGGA	AGTCTACAAA	TTGAAGTCCC	TTGGATTAAAC	TCAGTAACGA	GGTCTGTAAC
	241	TTGCTTTGAA	CCCACATATAT	TNNNNNNNCT	CGGGCAATGA	CTCAGTGTTGG	CAAGGATACT
		AACGAAACTT	GGGTGATATA	ANNNNNNNGA	GCCCGTTACT	GAGTCACACC	GTTCTTATGA
	301	ACTGCAGGCC	TGTTTCTGGA	AGGCACIGGA	CTCCTCTGAT	GCAAACCTTG	GCCAGGGACT
		TGACGTCGGG	ACAPAGACCT	TCCGTGACCT	GAGGAGACTA	CGTTTGAAC	CGGTCCCTGA
	361	CCTTGATAGC	TCTTAAATAG	ATGCTGCACC	AACACTCTCT	TTCTTTTCTC	TCTTTTCTT
		GGAACATATCG	AGAATTATC	TACGACGTGG	TTGTGAGAGA	AAGAAAGAG	AGAAAAGAA

123/130

FIG. 78B

421 TATTCAATAT TAGACTACAA GCAGTCTNAG GACTTCTCAG GGTTCCTAGC TCTCTCTCAT
ATAAGTTATA ATCTGATGTT CGTCAGATTG CTGAGAGATC CCAAGATCG AGAGAGAGTA

481 TTCACACATG CTTTCCTAGT AATCTCTACT CAIATATCTT ACTGCTACGC TGGGGCCAGA
AAGTGTGTAC GAAAGGATCA TTAGAGATGA GTATATAGAA TGACGATGCG ACCCCGGTCT

541 TAACNNNNNN CTTCCATTTT GTTTTATCTT CTATTCITCT TCCCCTTCTG CTTTCATTAT
ATTGNNNNNN GAAGGTAAAA CAAAATAGA GATAAGAAGA AGGGGAAGAC GAAAGTAATA

601 TGAACCTTC TGCTTTCATT ATTGAAACTT TCCCAGATTG GTTCTGCTTA ACCTGGCATT
ACTTTGAAAG ACGAAAGTAA TAACTTTGAA AGGTCTTAA CAAGACGAAT TGGACCGTAA

661 GGAACGTGTT CCTCTTCCCT GTGCTGCTTT CTCCCATTGC CATGTCCTTT TTTTTTTTTT
CCTTGACAAA GGAGAAGGGA CACGACGAAA GAGGGTAAAG GTACAGGAAA AAAAAAAAAA

721 TTTTTTTTTT TGAGACAGTG TCACTCTGTT GCCCAGGCTG GAGTGCAATG GTGCAATCTT
AAAAAAAAAA ACTCTGTCAC AGTGAGACAA CGGGTCCGAC CTCACGTTAC CACGTTAGAA

124/130

FIG. 78C

781 GCCCACTGCA ACCCCGCGCT CCCGGGTTC AAGTATTCTC CTGCCTCAGC CTCTGAGTA
CCGGIGACGT TGGGGGCGGA GGGCCCAAGT TCACTAAGAG GACGGAGTCG GAGGACTCAT

841 GCTGGGATTA CAGGTGCCCCA CCACTATGCC CGGCTGATT TTGTATTTT AGTAGAGATN
CGACCCTAAT GTCCACGGGT GGTGATACGG GCGGACTAAA AACATAAAA TCATCTCTAN

901 NNNNNNTTT CACCATNGCT GATCAGGCTG GTCTCGAACT CCTGACCGCA GTGANTCCGC
NNNNNNNAAA GTGGTANCGA CTAGTCCGAC CAGAGCTTGA GGAAGTGGGT CACTNAGGCG

961 CCTCCTTGGC CTCCCAGGT GCTGAGATTA CAGGCATGAG TCACTGCGNC CAUCCACCAT
GGAGGAACCG GAGGGTTTCA CGACTCTAAT GTCCGTACTC AGTGACGCG GTGCGTGCTA

1021 TATTCTCTAG AGGTGAGAGA ACACGTGGCTC TTCTAACAG TTGAAATTG ATAGAGACC
ATAAGAGATC TCCACTCTCT TGTGACCGAG AAGATTGTTT CACTTTAAG TATCTCTG

125/130

FIG. 79A

10	20	30	40	50	60	
1	CACAAAAA	GATTATTAGC	CACAAAAA	CCTTGAAGTA	ACGCATTAA	ATGTTAATGG
	GTGTTTTTTT	CTAATAATCG	GTGTTTTTTT	GGAACCTCAT	TGCSTAATTT	TACAATTACC
61	ATTCACTTTA	TTGAGCATCT	GCTCATAATA	CTTTAATGAG	TGCAAAAGTGC	TTTGAATATA
	TAAGTGAAAT	AACTCGTAGA	CGAGTATTAT	GAAATTACTC	ACGTTTCACG	AAACTTATAT
121	ATACGTCAAT	TAAACCTTAC	CATAATTCIG	AGGAATTGCT	ACCTCCACTT	CACAGATGGG
	TATGCAGTAA	ATTGGAATG	GIATTAAGAC	TCCTTAAACGA	TGGAGGTGAA	GTGTCCTACCC
181	GCACAGGAGG	CTTAGATAAC	ATGCCCAAG	TCATGCTTCT	AGTAAATGGA	TATAATTAAAG
	CGTGTCCTCC	GAATCTATTG	TACGGGTTTC	AGTACGAAGA	TCATTTACCT	ATATTAAATTC
241	ATTCAAATTA	TTGATAAGAA	TTTGATCTGC	CTTACCAGTA	TCTAGTAGTA	AATCTAAAG
	TAAGTTTAAT	AACTATTCTT	AACTAGACG	GAAATGGTCAT	AGATCATCAT	TTAGATTTTC
301	CGCTTTCCAG	AGCATGTGCT	GTTGATAGAG	CTTGATGCT	AACTCTCTGA	AATTTTCCAT
	GCGAAAGGTC	TCGTACACGA	CAACTATCTC	GAACTACAGA	TTGAGAGACT	TTAAAGGTA
361	TCTTATTGT	CTCACTGGTA	TATAGTTATT	TTTTACTACT	TTCATACACC	TACTAAGAG
	AGAATAAACA	GAGTGACCAT	ATATCAATAA	AAATGATGA	AAGTATGTGG	ATGATTCCTC

126/130

FIG. 79B

421 ACAGGAGGAT CAAAGATAGG ATTTCATTTA GAATGCCCTAA AGCTTCACGT ATTTAAATTC
TGTCCTCCTA GTTCTATCC TAAAGTAAAT CTTACGGATT TCGAAGTGCA TAAATTTAAG

481 AGAATAAGAT TCAGGCAGAC CACCAGTATA TGCCATGGTC CCTGGTTATC TTTCAGCAGG
TCTTATTCTA AGICCGTCTG GTGGTCATAT ACGGTACCAG GACCAATAG AAAGTCGTCC

541 TGACCGAGAA AGAAACATG GTAATGTITA TGAATGGTG GGTCTTGTA GTTTCACCTC
ACTGGCTCTT TCTTTGTAC CATTACAAAT ACTTIACCAC CCAAGAACAT CAAAGTGAAG

601 AACATACTG CCTTTACIGT ATTAAGATGA TGGATTAACT TATCTTGAT ATGGGCATGT
TTGTATAGAC GGAATGACA TAATICTACT ACCTAATTGA ATAAGAACTA TACCCGTACA

661 AAACAATAT ACTTTTACTA AACAGCTACA GAGAGACAAA TGTGTTTCCA GACAAACTTA
TTTTGTATA TGAAATGAT TTGTCGATGT CTCTCTGTTT ACACAAAGGT CTGTTTGAAT

721 AGAGACTGAG TGTTCAACT GAATAATCTC GACCTTAATT GAACTATAT TTATGAAAT
TCTCTGACTC ACAAGTTTGA CTTATTAGAG CTGGAATTAA CATTGATATA AAATACTTTA

127/130

FIG. 79C

781 CCAGCTGTAA GGC AAAACA GACTTCTTTG GGCTACCAC GGGCATTTTG TTCTGT TAN
GGTCGACATT CCGTTTTTGT CTGAAGAAC CCGATGGTG CCGTAAAC AGGACAATN

841 NNNACTCCA AACCTTAAC CCACGTCCAC TTAAATRAIG GCCTGGAAAT AAATGTCATT
NNNATGAGGT TTGGAATTG GGTGCAGGTG AATTATTAC CGACCTTTA TTACAGTAA

901 ATCIGATATT ATACTGAGAT GTTAGTTAT GAATCAAA GTGGAGAAT TCAATCTGTC
TAGACTATAA TATGACTCTA CAAACNATA CTTAGTTTT CACCTCTTAA AGTTAGACAG

961 CTGTAAGCTT TCTCTGGGT CACGACCCIC ATGCACTCAG GCTGTGCGGT GCAGCATGCT
GACATTGGA AGAGACGCCA GTGCTGGAG TAGGTGAGTC CGACACGCCA CGTCGTACGA

1021 CTGTCATGTC TGTCTCTTC TGCCTGTACA CGGGTGGTTG TTCTGTCTA CCTGTTTGAG
GACAGTACAG ACNAAAGAAG ACGACATGT GCCCACCAC AACGACAGAT GGACAACTC

1081 GAAATATGAA TACGTNNNN NCTAGAATCT ACTGCACATG CAATAAGGAA ACAATCAGTA
CTTTTACTT ATGCANNNN NGATCTTAGA TGACGTGTAC GTTATTCCTT TGTAGTCAT

1141 AGAATCACTT TCTCGTGGAA AATTCATTAG AATTAACATC TCGTTTTAAA ATGCTCTATC
TCTTAGTGAA AGAGCACCTT TTAAGTAAATC TTAATTGTAG AGCAAAATTT TACGAGATAG

128/130

FIG. 79D

1201 AAAGTGTAAG TAATTCCTCT CTCCTTTCCC TTTTCACTA AGGAGTTTGT ATATTAACA
TTTCACATTT ATTAAGGAGA GAGAAAGGG AAAAGTGAT TCCTCAAACA TATAATTGT

1261 GAATTTCAG TAATGTATTA TAAATTTATT TAANNATTT ACAATAAAT GCCACGTATA
CTTAAAGTTC ATTACATAAT ATTAAATAA ATNNATAAA TOTTATTTTA CCGTGCAAT

1321 AGCATCAAGC AACATGANN NNNCATTTGGT AGAAGCACA ATACATAGTC AAAACAGCAG
TCGTAGTTTG TTGTACTNNN NNGTAACCA TCTTTCGTGT TATGTATCAG TTTTGTGTC

1381 AGTATTAAAT AAACAGAAAA TTTGCAAAAG GCAAGTAAAG AATATACATA TACTTAATTA
TCATAATTTA TTTGTCTTTT AAACGTTTTC CTTTCATTTC TTATATGTAT ATGAATTAAT

1441 TACATAAAAT ATTGATACAG GAGGTAGAAA GAAATTTAGT AAGCAGATAA TGGGGGCAAC
ATGTATTTTA TAACTATGTC CTCATCTTT CTTTAAATCA TTCGTCTATT ACCCCCGTTG

1501 AGAGTCCTCA GCAGAGCTTC CCTTCTAACA AAAAGCAGCC CAATAAATTA TTTTTTTTTT
TCTCAGGAGT CGTCTCGAAG GGAAGATTGT TTTTCGTGCG GTTATTTAAT AAAAAA

1561 CTAACAAAA GCAGCCCTGAA AATCGAGCT GCAACATAG ATTAGCAATC GGCTGAAAGT

129/130

FIG. 79E

GATTGTTTTT CGTCGGACTT TTTAGCTCGA CGTTTGTATC TAATCGTTAG CCGACTTTCA

1621 GCGGGAGAAT GCTGGCAGCT GTGCCAATAG TAAAGGGCIA CCTGGAGCCG GCGCGGTGGC
CGCCCTCTTA CGACCGTCGA CACGGTTATC ATTCCCGAT GGACCTCGGC CCGCGCACCG

1681 TCACGCTGTA ATCCAGCAC TTTGGGAGGG CGAGGCAACG CGATCACCT GAGTCCGGA
AGTGGGACAT TAGGGTCGTG AAACCTCCC GCTCCGTGC GCCTAGTGA CTCCAGCCCT

1741 GTTTGAGATC AGCCGACCA ACATGGAGAA ACCCGTCTC TACTAATAA AAAAAAAAA
CAAACTCTAG TCGGGCTGGT TGTACCTCTT TGGGCGAGAG ATGATTTTTT TTTTTTTTTT

1801 AAAGGCAAAA AATGAGCCGG GCATGGTGGC ACATGCCCTG CACATCCCAG CTGAGGCAGG
TTTCCGTTTT TTAATCGGCC CGTACCACCG TGTACGGNAC GTGTAGGTC GACTCCGTCC

1861 AGAATCACT TGAACCTGGG AGGTAGAGAT TCGGTGAAG CGAGATCAG TCATTGCCACT
TCCTAAGTGA ACTTGGACCC TCCATCTCTA AGCCACTTC GCTCTAGTGC AGTAACGTGA

1921 CCAGCCTGGG CAAAAGAGC AAACCTAGT CTCAAAAAA AAAAAAAAA GAAAAA
GGTCGGACCC GTTTTCTCG TTTTGAATCA GAGTTTTTT TTTTNGTTT CTTTTT

130/130

FIG. 80

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